

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 17:51:32 : Search time 85 Seconds
(without alignments)
760.020 Million cell updates/sec

Title: US-10-017-372E-37

Perfect score: 2159

Sequence: 1 MAPSGLRLPLLLPLMLLV.....GRPKVEQLSNMIVRSCKKS 407

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Listing first 45 summaries

Database : A_Geneseq_19Jun03.*

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24: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

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Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2048.5	94.9	390	AAE13596	Porcine transform
2	1926.5	89.2	390	AA039186	Human polypeptide
3	1919.5	88.9	390	PAP61468	PreTGF-beta gene p
4	1919.5	88.9	390	11 AAR04034	Sequence of pre-TG
5	1919.5	88.9	390	11 AAR05258	Human pre-transfor
6	1919.5	88.9	390	12 AAR13813	Human pro-TGF-beta
7	1919.5	88.9	390	16 AAR73596	Human TGF-beta 1 p
8	1919.5	88.9	390	17 AAR90827	Pre-transforming g
9	1916.5	88.8	390	23 AAU77101	Human transforming

10	1916.5	88.8	390	23	AAE16943	Human transforming
11	1916	88.7	391	24	ABB82780	TGFβ1 Arg25Pro pol
12	1914.5	88.7	390	13	AAE20124	Sequence of simian
13	1910.5	88.5	390	15	AAE46227	Human pre-TGF-beta
14	1909	88.4	391	16	AAE83034	Transforming growt
15	1908.5	88.4	390	19	AAW78785	Human pre-transfor
16	1907.5	88.4	390	22	AAE84601	Nucleotide sequenc
17	1905	88.2	391	9	AAE81362	Human transforming
18	1904	88.2	434	11	AAE03743	Monkey transforming
19	1900.5	88.0	390	24	ABB82781	TGFβ1 Arg25Pro pol
20	1883.5	87.2	385	11	AAE05683	Simian Transformin
21	1878	87.0	387	11	AAE05684	Simian Transformin
22	1867.5	86.5	390	11	AAE05452	Chimeric simian TG
23	1863.5	86.3	390	13	AAE27522	TGF-beta 1/beta 2
24	1844	85.4	389	13	AAE29657	TGF-beta 1. Homo
25	1839	85.2	453	22	AAE40972	Human polypeptide
26	1758.5	81.4	390	13	AAE012541	Sequence of hybrid
27	1757.5	81.4	390	11	AAE05749	Human transforming
28	1751.5	81.1	390	11	AAE05685	Human TGF-beta2 ex
29	1749.5	81.0	390	11	AAE05686	Human transforming
30	1742	80.7	391	10	AAE91900	Hybrid transformin
31	1715	79.4	389	16	AAE79921	Sequence encoded b
32	1300	60.2	278	15	AAE53090	Simian-human hybr1
33	1295	60.0	278	12	AAE12541	Polypeptide cross-
34	1262.5	58.5	458	23	ABG31507	Latency associated
35	1262.5	58.5	463	23	ABG31510	LAP-miFNB construc
36	1169	54.1	290	22	ABG06792	LAP-huIFNB construc
37	1135	52.6	450	23	ABG31508	Novel human diagno
38	1128	51.8	448	23	ABG31509	miFNB-LAP construc
39	944	43.7	227	22	ABG20234	huIFNB-LAP construc
40	901	41.7	236	22	ABG20233	Novel human diagno
41	868.5	40.2	382	21	AAE08338	Amino acid sequenc
42	868.5	40.2	382	23	AAU77105	Frog transforming
43	832.5	38.6	456	13	AAW78786	Pig transforming g
44	828.5	38.4	412	16	AAE73598	Human TGF-beta 3 p
45	826	38.3	456	15	AAE46228	Pig TGF-beta-3. S

ALIGNMENTS

RESULT 1
AAE13596
ID AAE13596 standard; Protein; 390 AA.

XX AC AAE13596;

XX DT 26-FEB-2002 (first entry)

XX DE Porcine transforming growth factor beta 1 (TGF-beta1) mutant.

XX KW Porcine; transforming growth factor beta 1; TGF-beta1; gene therapy;
KW IBD; inflammatory bowel disease; autoimmune disease; immunosuppressive;
KW multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
KW diabetes mellitus; sarcoidosis; psoriasis; dermatological; mutant;
KW mutain.

XX OS Sus scrofa.

XX FH Key Location/Qualifiers

FT Misc-difference 223 /note= "Wild type Cys substituted with Ser"

FT Misc-difference 225 /note= "Wild type Cys substituted with Ser"

XX FT WO200181404-A2.

XX PD 01-NOV-2001.

XX PF 20-APR-2001; 2001WO-US12980.

XX PR 20-APR-2000; 2000US-199014P.

XX XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Strober W, Nakamura K, Kitani A, Fuss LJ;

XX WPI: 2002-026155/03.

DR N-PSDB; AAD22696.

XX Composition for treating autoimmune diseases e.g. inflammatory bowel
PT disease in humans, comprises vector containing transforming growth
PT factor-beta under the control of inducible promoter -

XX Example 1: Fig 1; 78pp: English.

XX The invention relates to a composition containing a vector comprising a
CC gene encoding a regulatory transcription factor under the control of a
CC promoter encoding a transforming growth factor-beta (TGF-beta). The
CC vector is useful for expressing TGF-beta, such as TGF-beta1, TGF-beta2
CC or TGF-beta3, its variants or homologues, by transfecting a cell which
CC is part of a host suspected of having an autoimmune disease, especially
CC inflammatory bowel disease (IBD), under conditions such that the
CC polypeptide encoded by the nucleic acid sequence in the vector is
CC expressed. The vector is delivered using a delivery system. The delivery
CC of the vector results in substantial elimination of symptoms of the
CC autoimmune disease and increased production of IL-10 by the host. The
CC composition is useful for treating various diseases with an autoimmune
CC component such as multiple sclerosis, rheumatoid arthritis, systemic
CC lupus erythematosus, insulin-dependent diabetes mellitus, sarcoidosis
CC and psoriasis, and also for assaying the expression of a gene in a cell.
CC The vector is further useful for screening of the effect of test
CC compounds on cytokine (e.g. TGF-beta) expression of transfected cells.
CC The present sequence is porcine TGF-beta1 mutant.

XX Sequence 390 AA;

Query Match 94.9%; Score 2048.5; DB 23; Length 390;

Best Local Similarity 95.8%; Pred. No. 5.2e-171;

Matches 390; Conservative 0; Mismatches 0; Indels 17; Gaps 1;

QY 1 MAPSGRLRLPLLLPLLLVLTGPPAAGLSTCKTIDMELVKRRKRIEIRGOILSKRLA 60
DB 1 MAPSGRLRLPLLLPLLLVLTGPPAAGLSTCKTIDMELVKRRKRIEIRGOILSKRLA 60
QY 61 SPSSQGVPPGPPLEAVLALNSTDRVAGESVEPEPEADYAKETRYVLMVYESNQI 120
DB 61 SPSSQGVPPGPPLEAVLALNSTDRVAGESVEPEPEADYAKETRYVLMVYESNQI 120
QY 121 YDKFKGTPLSLYMLFNTSFLHEAVPEPVLSSRAELRLRLKVEQHYELKQYNSDSWR 180
DB 121 YDKFKGTPLSLYMLFNTSELREAVPEPVLSSRAELRLRLKVEQHYELKQYNSDSWR 180
QY 181 YLSNRLAPSDSPWLSFDVYGVVROWITRREAIEGFRLSAHSDDSKDNTLHVEINGFN 240
DB 181 YLSNRLAPSDSPWLSFDVYGVVROWITRREAIEGFRLSAHSDDSKDNTLHVEINGFN 240
QY 241 SGRRGLATIHGMNRPFLILNATPLERAOHLSSRRRALDTNSYPYDVPDYASLADTN 300
DB 241 SGRRGLATIHGMNRPFLILNATPLERAOHLSSRRRALDTNSYPYDVPDYASLADTN 300
QY 301 YCFSSSTEKNCCVQYIDFRKDLGKWIHEPKGYHANFCLGCPYIWSLDYQYSKVIALY 360
DB 284 YCFSSSTEKNCCVQYIDFRKDLGKWIHEPKGYHANFCLGCPYIWSLDYQYSKVIALY 343
QY 361 NOHNPASAPCCVQYIDFRKDLGKWIHEPKGYHANFCLGCPYIWSLDYQYSKVIALY 407
DB 344 NOHNPASAPCCVQYIDFRKDLGKWIHEPKGYHANFCLGCPYIWSLDYQYSKVIALY 390

RESULT 2

AA39186

ID AAM39186 standard; Protein; 390 AA.

XX

AC AAM39186;

XX

DT 22-OCT-2001 (first entry)

XX Human polypeptide SEQ ID NO 2331.

XX Human; nontropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.

XX Homo sapiens.

XX WO200153312-A1.

XX 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US34263.

XX 21-JAN-2000; 2000US-0488725.

XX 25-APR-2000; 2000US-0552317.

XX 09-JUL-2000; 2000US-0598042.

XX 19-JUL-2000; 2000US-0620312.

XX 03-AUG-2000; 2000US-0653450.

XX 14-SEP-2000; 2000US-0662191.

XX 19-OCT-2000; 2000US-0693036.

XX 29-NOV-2000; 2000US-0727344.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;

XX Zhao QA, Zhou P, Goodrich R, Drmanac RT;

XX WPI: 2001-442253/47.

XX N-PSDB; AAI58342.

XX Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -

XX Example 4; SEQ ID NO 2331; 10078pp: English.

XX The invention relates to human nucleic acids (AAI57798-AAI61369) and
CC the encoded polypeptides (AAM38642-AAI42213) with nontropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.

CC Note: The sequence data for this patent did not form part of the printed
CC specification.

XX Sequence 390 AA;

XX Query Match 89.2%; Score 1926.5; DB 22; Length 390;

XX Best Local Similarity 89.9%; Pred. No. 2.6e-160;

XX Matches 366; Conservative 10; Mismatches 14; Indels 17; Gaps 1;

QY 1 MAPSGRLRLPLLLPLLLVLTGPPAAGLSTCKTIDMELVKRRKRIEIRGOILSKRLA 60

DB 1 MPSPGRLRLPLLLPLLLVLTGPPAAGLSTCKTIDMELVKRRKRIEIRGOILSKRLA 60

QY 61 SPSSQGVPPGPPLEAVLALNSTDRVAGESVEPEPEADYAKETRYVLMVYESNQI 120

DB 61 SPSSQGVPPGPPLEAVLALNSTDRVAGESVEPEPEADYAKETRYVLMVYESNQI 120

QY 121 YDKFKGTSPHSYMLFNTSELREAVPEVLLSRAELRLRLKLVKQHVLYQKYSNDSWR 180
DB 121 YDKFKGTSPHSYMLFNTSELREAVPEVLLSRAELRLRLKLVKQHVLYQKYSNDSWR 180
QY 181 YLSNRLAPSDSPWLSFCVTGVVROWLTTRREALTEGFRLSAHSSSDSKDNTLHVEINGEN 240
DB 181 YLSNRLAPSDSPWLSFCVTGVVROWLTTRREALTEGFRLSAHSSSDSKDNTLHVEINGEN 240
QY 241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRRRALDNTNSYPYDVPDYASLALDTN 300
DB 241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRRRALDNTNSYPYDVPDYASLALDTN 300
QY 301 YCFSTERNCCVRQLYIDFRKDLGKWKIHEPKGYHANFCLGCPYIWSLDTQYSKVLALY 360
DB 284 YCFSTERNCCVRQLYIDFRKDLGKWKIHEPKGYHANFCLGCPYIWSLDTQYSKVLALY 343
QY 361 NOHNPASAPCCVPOALEPLPIVYVGRKPKVEQLSNMIVRSCKCS 407
DB 344 NOHNPASAPCCVPOALEPLPIVYVGRKPKVEQLSNMIVRSCKCS 390

RESULT 3
AAP61468
ID AAP61468 standard; Protein; 390 AA.
XX
AC AAP61468;
XX
DT 31-OCT-2002 (updated)
DT 28-OCT-1991 (first entry)
XX
DE PrefGF-beta gene product.
XX
KW Transforming growth factor beta; cancer; wound healing.
XX
OS Unidentified.
XX
FH Key
FT Protein
XX
XX
PN EP200341-A.
XX
PD 10-DEC-1986.
XX
PF 21-MAR-1986; 86EP-0302112.
XX
PR 22-MAR-1985; 85US-0715142.
PR 13-MAR-1987; 87US-0025423.
XX
PA (GETH) GENENTECH INC.
XX
PI Derynck RMA;
XX
DR WPI; 1986-326875/50.
DR N-PSDB; AAN60572.
XX
PT TGF-beta prodn. from transformed hosts - useful esp. for treating
PT wounds (J6 2/9/86).
XX
PS Disclosure; Fig 1b; 26pp; English.
XX
CC The gene product is known to stimulate cell proliferation and
CC inhibit anchorage-dependent growth of a variety of human cancer cell
CC lines, it is esp. useful in treatment of burns and the promotion of
CC surface and internal wound healing. TGF-beta may be expressed from a
CC transformed CHO cell line.
CC (Updated on 31-OCT-2002 to add missing OS field.)
XX
SQ Sequence 390 AA;

Query Match 88.9%; Score 1919.5; DB 7; Length 390;
Best Local Similarity 89.7%; Pred. No. 1.1e-159;
Matches 365; Conservative 10; Mismatches 15; Indels 17; Gaps 1;

QY 1 MAPSGRLRLPLLLPLMLLVLTGCRPAAGLSTCKTIDMELVKRKRRIEATRGQILSKLRLA 60
DB 1 MPPSGRLRLPLLLPLMLLVLTGCRPAAGLSTCKTIDMELVKRKRRIEATRGQILSKLRLA 60
QY 61 SPPSGDVPVPGPLPEAVLALYNSTRDRVAGESVEPEPEADYYAKVETRVLMVYESNQI 120
DB 61 SPPSGDVPVPGPLPEAVLALYNSTRDRVAGESVEPEPEADYYAKVETRVLMVYESNQI 120
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DB 121 YDKFKGTSPHSYMLFNTSELREAVPEVLLSRAELRLRLKLVKQHVLYQKYSNDSWR 180
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DB 181 YLSNRLAPSDSPWLSFCVTGVVROWLTTRREALTEGFRLSAHSSSDSKDNTLHVEINGEN 240
QY 241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRRRALDNTNSYPYDVPDYASLALDTN 300
DB 241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRRRALDNTNSYPYDVPDYASLALDTN 300
QY 301 YCFSTERNCCVRQLYIDFRKDLGKWKIHEPKGYHANFCLGCPYIWSLDTQYSKVLALY 360
DB 284 YCFSTERNCCVRQLYIDFRKDLGKWKIHEPKGYHANFCLGCPYIWSLDTQYSKVLALY 343
QY 361 NOHNPASAPCCVPOALEPLPIVYVGRKPKVEQLSNMIVRSCKCS 407
DB 344 NOHNPASAPCCVPOALEPLPIVYVGRKPKVEQLSNMIVRSCKCS 390

RESULT 4
AAR04034
ID AAR04034 standard; protein; 390 AA.
XX
AC AAR04034;
XX
DT 25-MAR-2003 (updated)
DT 31-OCT-2002 (updated)
DT 31-MAY-1989 (first entry)
XX
DE Sequence of pre-TGF-beta 1.
XX
KW Transforming growth factor beta-3 (TGF beta 3); tumour cells; growth
KW inhibition.
XX
OS Homo sapiens.
XX
FH Key
FT CDS
XX
PN W08912101-A.
XX
PD 14-DEC-1989.
XX
PF 08-JUN-1988; 88WO-US01945.
XX
PR 08-JUN-1988; 88WO-US01945.
XX
PA (GETH) GENENTECH INC.
XX
PI Derynck RMA, Gooddel DV;
XX
DR WPI; 1990-007474/01.
DR N-PSDB; AAQ02815.
XX
PT Nucleotide sequence encoding transforming growth factor beta-3 used as a
PT probe, or to produce TGF beta 3, for inhibiting growth of certain normal
PT and neoplastic cells, eg A549.
XX
PS Disclosure; Fig. 2; 61pp; English.
XX
CC Sequence is an exon of transforming growth factor-beta 1 (pre-TGF-beta
CC 1) polypeptide and corresponds to AA's 288-338 of mature TGF-beta 1. The
CC nucleic acid encoding second subtype of TGF-beta (TGF-beta 3) is useful

CC as a probe or to produce TGF-beta 3 for inhibition of normal and
 CC neoplastic cell growth.
 CC (Updated on 31-OCT-2002 to add missing OS field.)
 CC (Updated on 25-MAR-2003 to correct PR field.)
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX Sequence 390 AA:

Query Match 88.9%; Score 1919.5; DB 11; Length 390;
 Best Local Similarity 89.7%; Pred. No. 1.1e-159;
 Matches 365; Conservative 10; Mismatches 15; Indels 17; Gaps 1;
 QY 1 MAPSGRLRLPLLLPLLLWLLVLTGPPAAGLSTCKTIDMELVKKRIEAIHQILSKRLA 60
 Db 1 MPSPGRLRLPLLLPLLLWLLVLTGPPAAGLSTCKTIDMELVKKRIEAIHQILSKRLA 60
 QY 61 SPSPQGDVPPGPLEAVLALYNSTRDRVAGESVEPEPEADYAKETVRLMVESGNOI 120
 Db 61 SPSPQGEVPPGPLEAVLALYNSTRDRVAGESAEPPEADYAKETVRLMVETHNEI 120
 QY 121 YDKFKGTSHLYMLFNTSELREAVPEPVLLSRAELRLRLKLVQEHVELYKYSNDSWR 180
 Db 121 YDKFKQSTHSIYMFNTSELREAVPEPVLLSRAELRLRLKLVQEHVELYKYSNDSWR 180
 QY 181 YLSNRLAPSDSPPEWLSFDVTGVVQWLRRAEIEGFRLSAHSDDSKDNTLHVEINGFN 240
 Db 181 YLSNRLAPSDSPPEWLSFDVTGVVQWLRRAEIEGFRLSAHSDDSKDNTLQVDINGFT 240
 QY 241 SGRGDLATIHGMNRPFLLLMATPLERAQHLSSRRRALDNTNSYPDVPDYASIALDTN 300
 Db 241 TGRGDLATIHGMNRPFLLLMATPLERAQHLSSRRRALDNTNSYPDVPDYASIALDTN 283
 QY 301 YCFSTSEKNCVRLQYIDFRKDLGKWKIHEPKGYHANFCLGCPYIWSLDTQYSKVLALY 360
 Db 284 YCFSTSEKNCVRLQYIDFRKDLGKWKIHEPKGYHANFCLGCPYIWSLDTQYSKVLALY 343
 QY 361 NOHNPASAPCCVPOALEPLPIVYVGRKPKVQELSNMIVRSCKS 407
 Db 344 NOHNPASAPCCVPOALEPLPIVYVGRKPKVQELSNMIVRSCKS 390

RESULT 5
 AAR05258
 ID AAR05258 standard; protein; 390 AA.
 AC AAR05258;
 XX
 XX 25-MAR-2003 (updated)
 DT 05-AUG-1990 (first entry)
 XX Human pre-transforming growth factor-beta-1 (pre-TGF-beta-1).
 DE Transforming growth factor-beta-1 (TGF-beta-1);
 KW neoplastic cell line inhibition;
 KW EGF-potentiated anchorage-independent growth.
 XX
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FH Peptide 1..278
 FT Protein 279..2011
 FT Domain 8..23
 FT /note="hydrophobic domain"
 FT Modified-site 82..84
 FT /note="potential N-glycosylation site"
 FT Modified-site 136..138
 FT /note="as above"
 FT Modified-site 176..178
 FT /note="as above"
 FT Cleavage-site 277..278
 FT /note="proteolytic cleavage site"
 XX
 PN US4886747-A.

XX 12-DEC-1989.
 PD
 XX 13-MAR-1987; 87US-0025423.
 PF
 XX 13-MAR-1987; 87US-0025423.
 PR
 XX 22-MAR-1985; 85US-0715142.
 PR
 XX (GETH) GENENTECH INC.
 PA Derynck RMA, Goeddel DV;
 XX
 PI WPI: 1990-051338/07.
 DR N-PSDB; AAQ93301.
 XX
 PT Nucleic acid encoding transforming growth factor-beta -
 PT cloned into expression vectors for expression in eukaryotic host
 PT cells for therapeutic use
 PS
 XX Disclosure; Fig 1b; 28pp; English.
 XX Pre-TGF-beta-1 is a polypeptide of 390 amino acids. Post-translational
 CC cleavage of the precursor gives rise to the mature TGF-beta monomer.
 CC The sequence for human TGF-beta was determined by direct amino acid
 CC sequence analysis and by deduction from the TGF-beta cDNA. It is
 CC capable of inducing EGF-potentiated anchorage-independent growth of
 CC target cell lines, and/or growth inhibition of neoplastic cell lines. It
 CC can be used for treating wounds, eg burns or epidermal ulcers.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 390 AA;
 Query Match 88.9%; Score 1919.5; DB 11; Length 390;
 Best Local Similarity 89.7%; Pred. No. 1.1e-159;
 Matches 365; Conservative 10; Mismatches 15; Indels 17; Gaps 1;
 QY 1 MAPSGRLRLPLLLPLLLWLLVLTGPPAAGLSTCKTIDMELVKKRIEAIHQILSKRLA 60
 Db 1 MPSPGRLRLPLLLPLLLWLLVLTGPPAAGLSTCKTIDMELVKKRIEAIHQILSKRLA 60
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 Db 61 SPSPQGEVPPGPLEAVLALYNSTRDRVAGESAEPPEADYAKETVRLMVETHNEI 120
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 Db 181 YLSNRLAPSDSPPEWLSFDVTGVVQWLRRAEIEGFRLSAHSDDSKDNTLQVDINGFT 240
 QY 241 SGRGDLATIHGMNRPFLLLMATPLERAQHLSSRRRALDNTNSYPDVPDYASIALDTN 300
 Db 241 TGRGDLATIHGMNRPFLLLMATPLERAQHLSSRRRALDNTNSYPDVPDYASIALDTN 283
 QY 301 YCFSTSEKNCVRLQYIDFRKDLGKWKIHEPKGYHANFCLGCPYIWSLDTQYSKVLALY 360
 Db 284 YCFSTSEKNCVRLQYIDFRKDLGKWKIHEPKGYHANFCLGCPYIWSLDTQYSKVLALY 343
 QY 361 NOHNPASAPCCVPOALEPLPIVYVGRKPKVQELSNMIVRSCKS 407
 Db 344 NOHNPASAPCCVPOALEPLPIVYVGRKPKVQELSNMIVRSCKS 390
 RESULT 6
 AAR13813
 ID AAR13813 standard; Protein; 390 AA.
 AC AAR13813;
 XX
 XX 20-NOV-1991 (first entry)
 DT
 XX

```

DE XX Human pro-TGF-beta 1.
KW XX Osteogenetic; tumoricidal.
XX XX Homo sapiens.
OS XX
XX XX Key Location/Qualifiers
FH FT Peptide 1..29
FT FT /note= "signal peptide"
FT FT 30..390
FT FT /note= "pro-TGF-beta 1"
FT FT 279..390
FT FT /note= "TGF beta 1"
XX XX
PN XX JP03180192-A.
XX XX
XX XX 06-AUG-1991.
XX XX
XX XX 07-DEC-1989; 89JP-0318243
XX XX
XX XX 07-DEC-1989; 89JP-0318243.
XX XX
XX XX (KIRI ) KIRIN BREWERY KK.
XX XX
XX XX WPI; 1991-271579/37.
DR XX N-PSDB; AAQ13392.
DR XX
XX XX Human pro-TGF-beta 1 prodn., for osteo-genetic activity - by
PT PT preparing DNA chain contg. base sequence coding for human
PT PT pre:pro-TGF-beta 1, forming expression vector etc.
XX XX
XX XX Claim 1; Fig 1; 16pp; Japanese.
XX XX
CC XX The amino acid sequence codes for human prepro-TGF-beta 1 which
CC CC can be produced by recombinant methods, it has osteogenetic and
CC CC tumoricidal activity.
XX XX
SQ XX Sequence 390 AA;

Query Match 88.9%; Score 1919.5; DB 12; Length 390;
Best Local Similarity 89.7%; Pred. No. 1.1e-159; Mismatches 15; Indels 17; Gaps 1;
Matches 365; Conservative 10;

QY 1 MAPSGLRLPLLLPLLMWLVLTGPPAAGLSTCKTIDMELVKRKRIRAEIRGQILSKRLA 60
DB 1 MPSPGLRLPLLLPLLMWLVLTGPPAAGLSTCKTIDMELVKRKRIRAEIRGQILSKRLA 60
QY 61 SPSPQGDVPPGPLEPAVLAALYNSTRDRVAGESVEPEPEADYYAKEVTRVLMWESGNOI 120
DB 61 SPSPQGEVPPGPLEPAVLAALYNSTRDRVAGESAEPEPEADYYAKEVTRVLMWETHNEI 120
QY 121 YDKFKGTSHSLYMLFNTSELREAVPEPVLLSRAELRLRLKLVQEHVELYQKYSNDSWR 180
DB 121 YDKFKQSTHSIYFFNTSELREAVPEPVLLSRAELRLRLKLVQEHVELYQKYSNNSWR 180
QY 181 YLSNRLAPSDSPWLSFDVTGVVROWLTRFRAIEGFRLSAHSSSDSKDNTLHVINGFN 240
DB 181 YLSNRLAPSDSPWLSFDVTGVVROWLTRFRAIEGFRLSAHSSDSDRNTLQVDINGFT 240
QY 241 SGRRGDLATHGNRRPFLIMATPLERAQHLHSSRRRALDNTNSYPDYPDYLALDTN 300
DB 241 TGRGDLATHGNRRPFLIMATPLERAQHLHSSRRR-----ALDTN 283
QY 301 YCFSSTEKNCVRLQYIDFRKDLGKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 360
DB 284 YCFSSTEKNCVRLQYIDFRKDLGKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 343
QY 361 NOHNPASAPCCVPOALEPLPIYIVYGRKPKVQELSNMIVRSCKS 407
DB 344 NOHNPASAPCCVPOALEPLPIYIVYGRKPKVQELSNMIVRSCKS 390

RESULT 7

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AAR73596
ID AAR73596 standard: Protein: 390 AA.
XX AC
XX AAR73596;
XX XX
DT 25-MAR-2003 (updated)
DT 20-DEC-1995 (first entry)
XX DE
XX Human TGF-beta 1 protein.
XX KW Transforming growth factor-beta: Human TGF-beta protein; TGF-beta 1;
KW TGF-beta 3; osteogenic cell source; OCS; bone deficiency;
KW bone-inducing cofactor.
XX OS Homo sapiens.
XX PN US5409896-A.
XX XX
PD 25-APR-1995.
XX XX
XX 12-NOV-1993; 93US-0132405.
XX XX
XX 01-SEP-1989; 89US-0401906.
XX 12-NOV-1991; 91US-0790856.
XX 18-MAY-1993; 93US-0063841.
XX 12-NOV-1993; 93US-0132405.
XX XX
XX (GETH ) GENENTECH INC.
XX XX
XX Ammann AJ, Rudman CG;
XX XX
XX WPI; 1995-169610/22.
XX XX
XX Compsn. for treating skeletal tissue deficiency - comprising
PT transforming growth factor-beta and an osteogenic cell source in a
PT carrier
XX XX
XX Claim 3; Column 15-18; 19pp; English.
XX XX
XX This sequence represents human transforming growth factor-beta 1
CC (TGF-beta 1). This sequence and the sequence for human TGF-beta 3 (see
CC AAR73598) are claimed within the scope of the invention. The invention
CC is a composition consisting of a TGF-beta protein and an osteogenic cell
CC source (OCS) formulated in an acceptable carrier other than a bone
CC morphogenic cofactor. This composition can be used for the restoration
CC of bone deficiency. This provides for the generation of mature bone
CC only where it is required, without the inclusion of a specific
CC bone-inducing cofactor. This method can be used with any of the 5 human
CC TGF-beta's or with TGF-beta from other species.
CC (Updated on 25-MAR-2003 to correct PF field.)
XX XX
SQ Sequence 390 AA;

Query Match 88.9%; Score 1919.5; DB 16; Length 390;
Best Local Similarity 89.7%; Pred. No. 1.1e-159; Mismatches 15; Indels 17; Gaps 1;
Matches 365; Conservative 10;

QY 1 MAPSGLRLPLLLPLLMWLVLTGPPAAGLSTCKTIDMELVKRKRIRAEIRGQILSKRLA 60
DB 1 MPSPGLRLPLLLPLLMWLVLTGPPAAGLSTCKTIDMELVKRKRIRAEIRGQILSKRLA 60
QY 61 SPSPQGDVPPGPLEPAVLAALYNSTRDRVAGESVEPEPEADYYAKEVTRVLMWESGNOI 120
DB 61 SPSPQGEVPPGPLEPAVLAALYNSTRDRVAGESAEPEPEADYYAKEVTRVLMWETHNEI 120
QY 121 YDKFKGTSHSLYMLFNTSELREAVPEPVLLSRAELRLRLKLVQEHVELYQKYSNDSWR 180
DB 121 YDKFKQSTHSIYFFNTSELREAVPEPVLLSRAELRLRLKLVQEHVELYQKYSNNSWR 180
QY 181 YLSNRLAPSDSPWLSFDVTGVVROWLTRFRAIEGFRLSAHSSSDSKDNTLHVINGFN 240
DB 181 YLSNRLAPSDSPWLSFDVTGVVROWLTRFRAIEGFRLSAHSSDSDRNTLQVDINGFT 240

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QY 241 SGRGDLATIHGMNRPFLLLMATPLERAQHLSSRRRALDTSYYPDYPDASALDNTN 300
 :|||||
 Db 241 TCRGDLATIHGMNRPFLLLMATPLERAQHLSSRRRALDTSYYPDYPDASALDNTN 283
 :|||||
 QY 301 YCFSTKNCVQRLYIDFRKDLGKWKIHEPKGYHANFCLGCPYIWSLDTOYSKVLALY 360
 :|||||
 Db 284 YCFSTKNCVQRLYIDFRKDLGKWKIHEPKGYHANFCLGCPYIWSLDTOYSKVLALY 343
 :|||||
 QY 361 NQNPASAPCCVPOALEPIPIVYVGRKPKVEQLSNMIVRSCKCS 407
 :|||||
 Db 344 NQNPASAPCCVPOALEPIPIVYVGRKPKVEQLSNMIVRSCKCS 390
 :|||||

RESULT 8
 AAR90827
 ID AAR90827 standard; Protein; 390 AA.
 XX
 AC AAR90827;
 XX
 DT 25-MAR-2003 (updated)
 DT 25-JAN-1980 (first entry)
 XX
 XX Pre-transforming growth factor beta 1.
 XX transforming growth factor beta 1; wound healing;
 KW recombinant production.
 KW
 OS Homo sapiens.
 XX
 FH Key
 FT Domain 8..23 Location/Qualifiers
 FT Modified-site 82..84 /note= "hydrophobic domain"
 FT Modified-site 136..138 /note= "potential N-glycosylation site"
 FT Modified-site 176..178 /note= "potential N-glycosylation site"
 FT Modified-site 277..279 /note= "potential N-glycosylation site"
 FT Cleavage-site 279..390 /note= "trypsin-like peptidase cleavage site"
 FT Protein /label= mature_TGF_beta_1

US5482851-A.

09-JAN-1996.

05-NOV-1993; 9305-0147364.

13-MAR-1987; 8705-0025423.

22-MAR-1985; 8505-0715142.

04-AUG-1989; 8905-0389929.

04-MAR-1992; 9205-0845893.

05-NOV-1993; 9305-0147364.

(GETH) GENENTECH INC.

Derynck RMA, Goeddel DV;

WPI; 1996-076891/08.

N-PSDB; AAT15720.

New recombinant human transforming growth factor-beta prods. - produced using Chinese hamster ovary cells, for use in diagnostic applications or in therapy

Example 3; Fig 1A-C; 26pp; English.

CC The pre-transforming growth factor (TGF) beta 1 protein is encoded by AAT15720. The mature TGF beta 1 monomer is cleaved from the precursor at the Arg-Arg dipeptide immediately preceding the mature TGF-beta 1 NH2-terminus. It does not contain a recognisable N-terminal signal peptide typical of most secreted proteins. The pre-TGF beta 1

CC contains several pairs of basic residues which could undergo post-translational cleavage and give rise to separate polypeptide entities. The precursor contains 3 potential N-glycosylation sites, none of which are localised in the mature TGF beta 1. This is useful in purification of the mature protein. TGF beta 1 can be used in, e.g. wound healing.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX

SQ Sequence 390 AA;

Query Match 88.9%; Score 1919.5; Db 17; Length 390;

Best Local Similarity 89.7%; Pred. No. 1; 159;

Matches 365; Conservative 10; Mismatches 15; Indels 17; Gaps 1;

QY 1 MAPSGLRLPLLLPLLLVLTGPPAAGLSTCKTIDMELVKRRIEATRGILSKRLA 60

Db 1 MPPSGLRLPLLLPLLLVLTGPPAAGLSTCKTIDMELVKRRIEATRGILSKRLA 60

QY 61 SPSPQGVPPGPLPEAVLALYNSTRVAGESVEPEPEPEADYAKETVRLMVESGNQI 120

Db 61 SPSPQGVPPGPLPEAVLALYNSTRVAGESVEPEPEPEADYAKETVRLMVETHNEI 120

QY 121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLRLKLVQHVELYQKYSNDSWR 180

Db 121 YDKFKGTTHSIYMFNTSELREAVPEPVLLSRAELRLRLKLVQHVELYQKYSNDSWR 180

QY 181 YLSNRLPLAPSDPEWLSFDVTGVVROWLITRRRAIEGFRLSAHSDDSKDNTLHVINGFN 240

Db 181 YLSNRLPLAPSDPEWLSFDVTGVVROWLITRRRAIEGFRLSAHSDDSKDNTLHVINGFT 240

QY 241 SGRGDLATIHGMNRPFLLLMATPLERAQHLSSRRRALDTSYYPDYPDASALDNTN 300

Db 241 TCRGDLATIHGMNRPFLLLMATPLERAQHLSSRRRALDTSYYPDYPDASALDNTN 283

QY 301 YCFSTKNCVQRLYIDFRKDLGKWKIHEPKGYHANFCLGCPYIWSLDTOYSKVLALY 360

Db 284 YCFSTKNCVQRLYIDFRKDLGKWKIHEPKGYHANFCLGCPYIWSLDTOYSKVLALY 343

QY 361 NQNPASAPCCVPOALEPIPIVYVGRKPKVEQLSNMIVRSCKCS 407

Db 344 NQNPASAPCCVPOALEPIPIVYVGRKPKVEQLSNMIVRSCKCS 390

:|||||

RESULT 9

AAU77101

ID AAU77101 standard; Protein; 390 AA.

XX

AC AAU77101;

DT 05-JUN-2002 (first entry)

DE Human transforming growth factor beta 1 (TGF-beta-1) polypeptide.

XX Human; transforming growth factor beta; TGF-beta; insulin production;

KW type I diabetes mellitus; pancreatic cell outgrowth; wound healing;

KW pancreatic duct tissue; ischaemia; stroke; nervous system aging;

KW neurological condition; neurodegenerative disease; inflammation;

KW nasal injury; chemical injury; traumatic injury; tumour-induced injury;

KW amyotrophic lateral sclerosis; spinocerebellar degeneration;

KW immunological disease; multiple sclerosis; TGF-beta-1.

OS Homo sapiens.

XX

PN WO200212336-A2.

XX

PD 14-FEB-2002.

XX

PF 09-FEB-2001; 2001WO-US04192.

XX

PR 09-AUG-2000; 2000US-0635368.

XX

PA (CURI-) CURIS INC.

XX

[illegible]

XX	Human; transforming growth factor-beta1; TGF-beta1; osteoporosis;
XX	latency associated peptide; LAP; integrin alphavbeta3; apoptosis;
XX	immunomodulation; inflammatory disease; fibrotic disease; cancer;
XX	diabetic retinopathy; chronic obstructive pulmonary disorder;
XX	bone resorption; rheumatoid arthritis; psoriasis; restenosis;
XX	atherosclerosis; liver fibrosis; asthma; cytostatic; osteopathic;
XX	ophthalmological; antiarteriosclerotic; vasotropic.
OS	Homo sapiens.
XX	
XX	Key Location/Qualifiers
FT	Peptide 1..29
FT	Region 30..278
FT	/note= "LAP-beta1"
FT	Domain 244..246
FT	/note= "RGD motif"
FT	Protein 279..390
FT	/note= "Human mature TGF-beta1 protein"
XX	
XX	WO200190186-A1.
PN	
PN	29-NOV-2001.
PD	
PD	
XX	
XX	25-MAY-2001; 2001WO-GB02352.
PF	
PF	
XX	
XX	26-MAY-2000; 2000GB-0012991.
PR	
PR	05-JAN-2001; 2001GB-0000286.
XX	
XX	(GLAX) GLAXO GROUP LTD.
PA	
PI	
PI	Ludbrook S, Barry S, Horgan C, Miller D;
DR	
DR	WPI; 2002-097645/13.
XX	
XX	Identifying modulators of interactions between latency associated
PT	peptides and integrin alphavbeta3 for therapeutics, by contacting the
PT	peptide and integrin with a test product and determining if the product
PT	modulates interaction .
PT	
PS	Disclosure; page 37-39; 44pp; English.
XX	
XX	The invention relates to a method for identification of a modulator
CC	of the interaction between latency associated peptide (LAP) of
CC	transforming growth factor-beta1 (TGF-beta1) and integrin alphavbeta3.
CC	The method is useful for identifying a modulator of the interaction
CC	between LAP and integrin alphavbeta3. The method is useful for
CC	immunomodulation, in the treatment of inflammatory disease, fibrotic
CC	disease, cancer, diabetic retinopathy, bone resorption or osteoporosis,
CC	and for preventing apoptosis administering the modulator to the host.
CC	The modulator (inhibitor of the interaction between LAP-beta1 and
CC	integrin alphavbeta3) is useful in the manufacture of a medicament for
CC	immunomodulation. The modulator (activator of the interaction between
CC	LAP-beta1 and integrin alphavbeta3) is useful in the manufacture of
CC	a medicament for preventing apoptosis. The modulator is useful for
CC	treating a inflammatory or fibrotic disease such as chronic obstructive
CC	pulmonary disorder, rheumatoid arthritis, psoriasis, restenosis, is
CC	atherosclerosis, liver fibrosis and asthma. The present sequence is
CC	human TGF-beta1 protein.
XX	
XX	Sequence 390 AA;
SQ	

[illegible]

Db 61 SPFGSGVPPGLPEAVLALYNSTRDRVAGESPEPEADYAKVETRVLMVETHNEI 120
 QY 121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRRAELRLRLKLVQEHVELYQKYSNDSWR 180
 Db 121 YDKFKGTSTHLYAFNTSELREAVPEPVLLSRRAELRLRLKLVQEHVELYQKYSNDSWR 180
 QY 181 YLSNRLAPSDSPFWLSFDVTGVVROWLTPREAEIEGFRLSAHSDDSKNTLHVEINGFN 240
 Db 181 YLSNRLAPSDSPFWLSFDVTGVVROWLTPREAEIEGFRLSAHSDDSKNTLHVEINGFN 240
 QY 241 SGRGGLDATTGHNRRPFLLLMATPLERAQHLHSSRRRALDTNSYDYPDVVASLALDTN 300
 Db 241 TGRGGLDATTGHNRRPFLLLMATPLERAQHLHSSRRRALDTNSYDYPDVVASLALDTN 283
 QY 301 YCFSSSTEKNCCVRLYIDFRKDLGKWIHEPKGYHANFCLGCPYIWSLDTQYSKVIALY 360
 Db 284 YCFSSSTEKNCCVRLYIDFRKDLGKWIHEPKGYHANFCLGCPYIWSLDTQYSKVIALY 343
 QY 361 NOHNPASAAAPCCVPQALEPLPIVYVGRKPKVEQLSNMIVRSCKCS 407
 Db 344 NOHNPASAAAPCCVPQALEPLPIVYVGRKPKVEQLSNMIVRSCKCS 390
 RESULT 11
 ABB82780
 ID ABB82780 standard; Protein; 391 AA.
 XX
 AC ABB82780;
 XX
 DT 18-MAR-2003 (first entry)
 XX
 TGFB1 Arg25Pro polymorphism G-allele protein sequence.
 DE
 KW Polymorphism; transforming growth factor beta 1; TGFB1; TGFbeta-1;
 KW renal failure; nephrotropic; human; allele.
 XX
 OS Homo sapiens.
 XX
 PN WO200290585-A2.
 XX
 PD 14-NOV-2002.
 XX
 PF 08-MAY-2002; 2002WO-GB02066.
 XX
 PR 09-MAY-2001; 2001GB-0011277.
 XX
 PA (UYSH-) UNIV SHEFFIELD HALLAM.
 XX
 PI El-Nahas AM, Blakemore A, Khalil MS;
 XX
 DR WPI; 2003-120560/11.
 DR N-PSDB; ABV75391.
 XX
 PT Determining an individual's susceptibility to the progression of renal
 PT failure comprises detecting the presence of a genetic polymorphism
 PT pattern in transforming growth factor beta 1 (TGFB1) gene in a sample
 PT from the individual -
 XX
 PS Claim 51; Page 59-61; 62pp; English.
 XX
 CC The invention relates to determining an individual's susceptibility to
 CC renal failure and involves detecting the presence of a genetic
 CC polymorphism pattern in transforming growth factor beta 1 (TGFB1) gene in
 CC a sample from an individual, where polymorphism pattern is associated
 CC with renal failure. The method is useful for determining an individual's
 CC susceptibility to the progression of renal failure. The nucleic acid
 CC comprising a T(-509)C polymorphism of TGFB1 gene, or a polypeptide
 CC comprising a sequence of 391 amino acids is useful for preparing a
 CC medicament for retarding or preventing the progression of renal disease,
 CC and for drug research purposes for retarding or preventing the
 CC progression of renal disease. Sequences ABV75386-88 represents the
 CC protein sequence for the TGFB1 G-allele of the Arg25Pro polymorphism
 CC of exon 1.

XX SQ Sequence 391 AA;
 Query Match 88.7%; Score 1916; DB 24; Length 391;
 Best Local Similarity 89.7%; Pred. No. 2.2e-159;
 Matches 366; Conservative 10; Mismatches 14; Indels 18; Gaps 2;
 QY 1 MAPSGRLRLPLLLPMLLVLTGPRPAAGLSTCKTIDMELVKRKRIEIRGOILSKRLA 60
 Db 1 MPPSGRLRLPLLLPMLLVLTGPRPAAGLSTCKTIDMELVKRKRIEIRGOILSKRLA 60
 QY 61 SPPSGOGVPPCPLEAVLALYNSTRDRVAGESPEPEADYAKVETRVLMVETHNEI 120
 Db 61 SPPSGOGVPPCPLEAVLALYNSTRDRVAGESPEPEADYAKVETRVLMVETHNEI 120
 QY 121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRRAELRLRLKLVQEHVELYQKYSNDSW 179
 Db 121 YDKFKGTSTHLYAFNTSELREAVPEPVLLSRRAELRLRLKLVQEHVELYQKYSNDSW 180
 QY 180 YLSNRLAPSDSPFWLSFDVTGVVROWLTPREAEIEGFRLSAHSDDSKNTLHVEINGFN 239
 Db 180 YLSNRLAPSDSPFWLSFDVTGVVROWLTPREAEIEGFRLSAHSDDSKNTLHVEINGFN 240
 QY 240 NSGRGGLDATTGHNRRPFLLLMATPLERAQHLHSSRRRALDTNSYDYPDVVASLALDT 299
 Db 241 TGRGGLDATTGHNRRPFLLLMATPLERAQHLHSSRRRALDTNSYDYPDVVASLALDT 283
 QY 300 NYCFSSSTEKNCCVRLYIDFRKDLGKWIHEPKGYHANFCLGCPYIWSLDTQYSKVIAL 359
 Db 284 NYCFSSSTEKNCCVRLYIDFRKDLGKWIHEPKGYHANFCLGCPYIWSLDTQYSKVIAL 343
 QY 360 YNOHNPASAAAPCCVPQALEPLPIVYVGRKPKVEQLSNMIVRSCKCS 407
 Db 344 YNOHNPASAAAPCCVPQALEPLPIVYVGRKPKVEQLSNMIVRSCKCS 391
 RESULT 12
 AAR20124
 ID AAR20124 standard; Protein; 390 AA.
 XX
 AC AAR20124;
 XX
 DT 25-MAR-2003 (updated)
 DT 16-APR-1992 (first entry)
 XX
 DE Sequence of simian transforming growth factor (TGF) beta-1.
 XX
 KW Hypertension therapy; hypotensive agent; blood pressure modulator.
 XX
 OS Monkey.
 XX
 FH Key Location/Qualifiers
 FT Peptide 8..21
 FT Protein 279..390
 XX
 PN WO9119513-A.
 XX
 PD 26-DEC-1991.
 XX
 PF 20-JUN-1991; 91WO-US04449.
 XX
 PR 20-JUN-1990; 90US-0541221.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Oleson FB, Comereshki CR;
 XX
 DR WPI; 1992-024199/03.
 DR N-PSDB; AAQ20289.
 XX
 PT Use of transforming growth factor (TGF)-beta and their
 PT antagonists - for modulating blood pressure, for treating
 PT hypertension and hypotension

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XX PS Disclosure; Fig 1: 42pp; English.
XX CC
CC CC A new method for treating hypertension comprises administering a
CC transforming growth factor (TGF)-beta to an individual at a dose
CC effective for lowering blood pressure; the TGF-beta may be e.g.
CC mature TGF-beta, a mature TGF-beta1/beta2 hybrid, TGF-
CC beta2 precursor, a latent TGF-beta2 precursor, hybrid TGF-beta1/TGF-
CC beta2 precursor, a latent TGF-beta1 complex or a latent TGF-beta2
CC complex.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX CC
XX SQ Sequence 390 AA:

Query Match      88.7%; Score 1914.5; DB 13; Length 390;
Best Local Similarity 89.4%; Pred. No. 2.9e-159;
Matches 364; Conservative 10; Mismatches 16; Indels 17; Gaps 1;

QY 1 MAPSGLRLPLLLVLTGCRPAAGLSTCKTIDMELVKRKRIEIRGQILSKRLA 60
DB 1 MPPSGLRLPLLLVLTGCRPAAGLSTCKTIDMELVKRKRIEIRGQILSKRLA 60
QY 61 SPSSQGDVPPGPLEPAVLALYNSTRDVAGESVEPEPEADYYAKEVTRVLVMSNQI 120
DB 61 SPSSQGDVPPGPLEPAVLALYNSTRDVAGESVEPEPEADYYAKEVTRVLVMSNQI 120
QY 121 YDKFKGTSPHLYMLFNTSELREAVPEPVLLSRALRLRLKLVQEHVELYQKYSNDSWR 180
DB 121 YDKFKGTSPHLYMLFNTSELREAVPEPVLLSRALRLRLKLVQEHVELYQKYSNDSWR 180
QY 181 YLSNRLAPSDSPWLSFDVTGVVROWLTRREAIEGFRLSAHSSDSDKNTLHVINGFN 240
DB 181 YLSNRLAPSDSPWLSFDVTGVVROWLTRREAIEGFRLSAHSSDSDKNTLHVINGFN 240
QY 241 SGRRGDLATHGMNRPFLMLMATPLERAQHLHSSRRALDNTNSYPDYDPAVASLADTN 300
DB 241 TGRRGDLATHGMNRPFLMLMATPLERAQHLQSSRRHR-----ALDIN 283
QY 301 YCFSTTEKNCCVRLYIDFRKDLGKWKIHEPKGYHANFCLGCPYIWSLDTQYSKVLY 360
DB 284 YCFSTTEKNCCVRLYIDFRKDLGKWKIHEPKGYHANFCLGCPYIWSLDTQYSKVLY 343
QY 361 NOHNPASAPCCVPOALEPIVYVYVGRKPKVEQLSNMIVRSCKS 407
DB 344 NOHNPASAPCCVPOALEPIVYVYVGRKPKVEQLSNMIVRSCKS 390

RESULT 13
AAR46227
ID AAR46227 standard; Protein; 390 AA.
XX AC
XX AC AAR46227;
XX DT
XX DT 25-MAR-2003 (updated)
XX DT 09-JUL-1994 (first entry)
XX DE
XX DE Human pre-TGF-beta-1.
KW TGF-beta-1; TGF-beta-2; transforming growth factor beta-1;
KW transforming growth factor beta-3; recombinant; wound healing;
KW vulnary.
XX OS Homo sapiens.
XX FH
XX FH Key Location/Qualifiers
XX FH Peptide 279..390
FT FT /label- Mat_peptide
FT FT 279
FT FT /note- "TGF-beta-1 release site"
FT FT 82..84
FT FT /label- N-glycosylation_site
FT FT 136..138
FT FT /label- N-glycosylation_site

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FT Modified-site 176..178
FT /label- N-glycosylation_site
XX US284763-A.
XX PN
XX PD
XX PD 08-FEB-1994.
XX PF
XX PF 04-MAR-1992; 92US-0845893.
XX PR
XX PR 22-MAR-1985; 85US-0713142.
XX PR 13-MAR-1987; 87US-0025423.
XX PR 04-AUG-1989; 89US-0389929.
XX PR 04-MAR-1992; 92US-0845893.
XX (GETH ) GENENTECH INC.
XX PA
XX PA Derynk RMA, Goeddel DV;
XX PI
XX PI WPI: 1994-056343/07.
XX DR
XX DR N-PSDB; AAQ56923.
XX PT
XX PT Nucleic acid sequences encoding transforming growth factor-beta -
XX diagnostic probes, and for use in therapeutics
XX PS
XX PS Disclosure; Fig 1b; 25pp; English.
XX CC
XX CC cDNA sequences were determined for human pre-TGF-beta-1 (AAQ56923),
XX plg TGF-beta-3 (AAQ56925) and human TGF-beta-3 (AAQ56926); and the
XX corresponding amino acid sequences were determined (AAR46227-29,
XX respectively). A genomic fragment corresponding to a human TGF-
XX beta-1 exon (AAQ56924) was also isolated and its amino acid sequence
XX determined (AAR46230). The sequences have been used in the
XX CC construction of vectors for the expression of recombinant TGF-
XX beta.
XX CC (Updated on 25-MAR-2003 to correct PF field.)
XX SQ
XX SQ Sequence 390 AA:

Query Match      88.5%; Score 1910.5; DB 15; Length 390;
Best Local Similarity 89.4%; Pred. No. 6.5e-159;
Matches 364; Conservative 10; Mismatches 16; Indels 17; Gaps 1;

QY 1 MAPSGLRLPLLLVLTGCRPAAGLSTCKTIDMELVKRKRIEIRGQILSKRLA 60
DB 1 MPPSGLRLPLLLVLTGCRPAAGLSTCKTIDMELVKRKRIEIRGQILSKRLA 60
QY 61 SPSSQGDVPPGPLEPAVLALYNSTRDVAGESVEPEPEADYYAKEVTRVLVMSNQI 120
DB 61 SPSSQGDVPPGPLEPAVLALYNSTRDVAGESVEPEPEADYYAKEVTRVLVMSNQI 120
QY 121 YDKFKGTSPHLYMLFNTSELREAVPEPVLLSRALRLRLKLVQEHVELYQKYSNDSWR 180
DB 121 YDKFKGTSPHLYMLFNTSELREAVPEPVLLSRALRLRLKLVQEHVELYQKYSNDSWR 180
QY 181 YLSNRLAPSDSPWLSFDVTGVVROWLTRREAIEGFRLSAHSSDSDKNTLHVINGFN 240
DB 181 YLSNRLAPSDSPWLSFDVTGVVROWLTRREAIEGFRLSAHSSDSDKNTLHVINGFN 240
QY 241 SGRRGDLATHGMNRPFLMLMATPLERAQHLHSSRRALDNTNSYPDYDPAVASLADTN 300
DB 241 TGRRGDLATHGMNRPFLMLMATPLERAQHLQSSRRHR-----ALDIN 283
QY 301 YCFSTTEKNCCVRLYIDFRKDLGKWKIHEPKGYHANFCLGCPYIWSLDTQYSKVLY 360
DB 284 YCFSTTEKNCCVRLYIDFRKDLGKWKIHEPKGYHANFCLGCPYIWSLDTQYSKVLY 343
QY 361 NOHNPASAPCCVPOALEPIVYVYVGRKPKVEQLSNMIVRSCKS 407
DB 344 NOHNPASAPCCVPOALEPIVYVYVGRKPKVEQLSNMIVRSCKS 390

RESULT 14
AAR83054

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ID	AAR83054	standard; Protein; 391 AA.
XX		
AC	AAR83054;	
XX		
DT	25-JUN-1996	(first entry)
XX		
DE	Transforming growth factor-beta 1.	
XX		
KW	macrophage inducible nitric oxide synthase; iNOS; constitutive NOS;	
KW	interleukin-1-beta; transforming growth factor-beta; TGF-beta; IL1-beta;	
KW	nitric oxide production; hypertension; inflammation; septic shock;	
KW	treatment.	
XX		
OS	Mammalian sp.	
XX		
FT	Key	Location/Qualifiers
FT	Protein	279..391
FT	/note=	'represents the mature active TGF beta-1 mol.*
XX		
PN	W09526745-A1.	
XX		
PD	12-OCT-1995.	
XX		
XX	05-APR-1994;	94WO-US03705.
XX		
PR	05-APR-1994;	94WO-US03705.
XX		
PA	(HARD) HARVARD COLLEGE.	
XX		
XX	Lee M, Perrella MA;	
XX		
XX	WPI; 1995-358443/46.	
DR	N-PSDB; AAT05876.	
DR		
XX		
PT	Treatment of hypertension, esp. in septic shock - by administering	
PT	transforming growth factor-beta e.g. to inhibit inducible nitric	
PT	oxide synthase gene transcription	
XX		
XX	Disclosure; Fig 17; 52pp; English.	
XX		
CC	Transforming growth factor-beta 1 (TGF-beta 1) has been found to inhibit	
CC	inducible nitric oxide synthase (iNOS) gene transcription, esp. in	
CC	interleukin-1-beta (IL1-beta) stimulated rat smooth muscle cells, and at	
CC	a dose which does not inhibit constitutive NOS. TGF-beta 1 or 2	
CC	(AAR83055) or their active fragments (esp. derived from the	
CC	carboxy-terminal 112 amino acids), can be used in the treatment of	
CC	hypertension, such as that associated with severe inflammation or septic	
CC	shock.	
XX		
PS	Sequence	391 AA;
XX		
Query Match	88.4%;	Score 1909; DB 16; Length 391;
Best Local Similarity	89.5%;	Pred. No. 8.9e-159;
Matches	365;	Conservative 10; Mismatches 15; Indels 18; Gaps 2;
QY	1	MAPSGRLRLPLLLPLLLVLTPGRPAAGLSTCKTIDMELVKRKRIEARGOILSKRLA 60
DB	1	MPPSGLRLPLLLPLLLVLTPGPPAAGLSTCKTIDMELVKRKRIEARGOILSKRLA 60
QY	61	SPPSOGDVPVPGPLPAVALALNSTRDRVAGESVEPEPEADYYAKEVTRVLVMSGNOI 120
DB	61	SPPSOGVEPPGPLPAVALALNSTRDRVAGESAEPEPEADYYAKEVTRVLVMTVTHEI 120
QY	121	YDKFKGTPHSLMYLNTSELREAVPEPVLLSRAELRL-RLALKVQHQVELYQKYSNDSW 179
DB	121	YDKFKQSTSIYMFNTSELREAVPEPVLLSRAELRLRLKLLKVEQHYELYQKYSNWS 180
QY	180	RYLSNRLAPSDSPWLVSFDVTGVVROWLVRREAIEGFRLSAHSDDSKDNTLHVEINGF 239
DB	181	RYLSNRLAPSDSPWLVSFDVTGVVROWLSRGEGIEGFRLSAHCSDSDNTLQVDINGF 240
QY	240	NSGRGDLATIHGMNRPFLLNATPLERAQHLHSRRRALDNTSPYDPVDPYASLALDT 299

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 18:00:32 ; Search time 10 Seconds
(without alignments)
574.017 Million cell updates/sec

Title: US-10-017-372E-37

Perfect score: 2159

Sequence: 1 MAPSGLRLPLLLPLLLV.....GRPKVEQLSNMIVRSCKCS 407

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 423.0858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued_Patents_NA:*

1: /cgn2_6/ptodata1/1/aa/5A_COMB.pap.*

2: /cgn2_6/ptodata1/1/aa/5B_COMB.pap.*

3: /cgn2_6/ptodata1/1/aa/6A_COMB.pap.*

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5: /cgn2_6/ptodata1/1/aa/PCrUS_COMB.pap.*

6: /cgn2_6/ptodata1/1/aa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1919.5	88.9	390	1	US-08-132-405-1
2	1919.5	88.9	390	1	US-08-395-939A-1
3	1919.5	88.9	390	5	PCT-US91-01861-1
4	1919.5	88.9	390	6	5168051-2
5	1914.5	88.7	390	1	US-07-669-171-2
6	1909	88.4	394	5	PCT-US94-03705-5
7	828.5	38.4	412	1	US-08-132-405-3
8	828.5	38.4	412	1	US-08-395-939A-3
9	824.5	38.2	412	4	US-09-380-662-21
10	824.5	38.2	412	5	PCT-US91-04541-2
11	824.5	38.2	412	6	5262319-2
12	823.5	38.1	410	5	PCT-US91-01861-3
13	809	37.5	414	1	US-08-132-405-2
14	809	37.5	414	1	US-08-395-939A-2
15	809	37.5	414	5	PCT-US94-03705-6
16	804	37.2	414	5	PCT-US91-01861-2
17	803	37.2	304	1	US-08-132-405-4
18	803	37.2	304	1	US-08-395-939A-4
19	803	37.2	304	5	PCT-US91-01861-4
20	802	37.1	414	6	5221620-4
21	800.5	37.1	455	6	5168051-11
22	793	36.7	442	6	5221620-2
23	753.5	34.9	139	4	US-08-065-844A-8
24	638	29.6	112	1	US-07-979-441-1
25	638	29.6	112	1	US-08-197-792-36
26	638	29.6	112	1	US-08-486-057B-41
27	638	29.6	112	1	US-08-459-850-36

28	638	29.6	112	1	US-08-459-214-36	Sequence 36, Appl
29	638	29.6	112	1	US-08-470-837-30	Sequence 30, Appl
30	638	29.6	112	2	US-08-789-588-41	Sequence 41, Appl
31	638	29.6	112	2	US-08-410-573-1	Sequence 1, Appl
32	638	29.6	112	3	US-09-123-233-2	Sequence 2, Appl
33	638	29.6	112	3	US-08-927-433-5	Sequence 5, Appl
34	638	29.6	112	4	US-08-868-452-30	Sequence 30, Appl
35	638	29.6	112	4	US-09-095-637D-1	Sequence 1, Appl
36	638	29.6	112	5	PCT-US93-03068-1	Sequence 1, Appl
37	638	29.6	114	1	US-08-481-377-23	Sequence 23, Appl
38	638	29.6	114	2	US-08-491-835-21	Sequence 21, Appl
39	638	29.6	114	3	US-09-153-733A-23	Sequence 23, Appl
40	638	29.6	114	3	US-08-946-092A-21	Sequence 21, Appl
41	638	29.6	114	3	US-09-172-062-21	Sequence 21, Appl
42	638	29.6	114	3	US-08-624-635-22	Sequence 22, Appl
43	638	29.6	114	4	US-09-301-520D-21	Sequence 21, Appl
44	638	29.6	114	4	US-09-389-705-23	Sequence 23, Appl
45	638	29.6	114	5	PCT-US94-00666-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1

US-08-132-405-1

; Sequence 1, Application US/08132405

; Patent No. 5409896

; GENERAL INFORMATION:

; APPLICANT: Ammann, Arthur J.

; APPLICANT: Rudman, Christopher G.

; TITLE OF INVENTION: Method of Inducing Bone Growth Using

; TITLE OF INVENTION: TGF-Beta

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/132,405

; FILING DATE: 06-OCT-1993

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/063841

; FILING DATE: 18-MAY-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/750856

; FILING DATE: 12-NOV-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/401906

; FILING DATE: 01-SEP-1989

; ATTORNEY/AGENT INFORMATION:

; NAME: Hasak, Janet E.

; REGISTRATION NUMBER: 28,616

; REFERENCE/DOCKET NUMBER: 597D1C2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-1896

; TELEFAX: 415/952-9881

; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 390 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

US-08-132-405-1


```

; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 537
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/266-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 390 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
;
PCT-US91-01861-1

Query Match      88.9%; Score 1919.5; DB 5; Length 390;
Best Local Similarity 89.7%; Pred. No. 3.7e-169;
Matches 365; Conservative 10; Mismatches 15; Indels 17; Gaps 1;

QY 1 MAPSGRLRLPLLLPLWLLVLTGPPAAGLSTCKTIDMELVKKRKEAIRGOILSKRLA 60
DB 1 MPFSGRLRLPLLLPLWLLVLTGPPAAGLSTCKTIDMELVKKRKEAIRGOILSKRLA 60
QY 61 SPFSGQGVPPGGLPEAVLALYNSTRDRVAGESVEPEPEADYYAKEVTRVLMVETNEI 120
DB 61 SPFSGQGVPPGGLPEAVLALYNSTRDRVAGESAEPEPEADYYAKEVTRVLMVETNEI 120
QY 121 YDFKGTPTISLYMLFNTSELREAVPEPVLLSRAELRLRLKLVKEQHVLYQKYSNDSWR 180
DB 121 YDFKGTPTISLYMLFNTSELREAVPEPVLLSRAELRLRLKLVKEQHVLYQKYSNDSWR 180
QY 121 YDFKGTSTHSIYMFNTSELREAVPEPVLLSRAELRLRLKLVKEQHVLYQKYSNDSWR 180
DB 121 YDFKGTSTHSIYMFNTSELREAVPEPVLLSRAELRLRLKLVKEQHVLYQKYSNDSWR 180
QY 181 YLSNRLAPSDSPWLSFDTGVVROWLTPRRAIEGFRLSAHSDDSKDNTLHVEINGFN 240
DB 181 YLSNRLAPSDSPWLSFDTGVVROWLTPRRAIEGFRLSAHSDDSKDNTLHVEINGFN 240
QY 241 SGRGDLATIHGMNRPFLLLMATPLERAOHLHSSRRRALDNTNSYPYDVPDYASLALDTN 300
DB 241 TGRGDLATIHGMNRPFLLLMATPLERAOHLHSSRRRALDNTNSYPYDVPDYASLALDTN 300
QY 301 YCFSSTEKNCCVRLYIDFRKDLGKWKIHEPKGYHANFCLGCPYIWSLDTQYSKVLALY 360
DB 284 YCFSSTEKNCCVRLYIDFRKDLGKWKIHEPKGYHANFCLGCPYIWSLDTQYSKVLALY 343
QY 361 NOHNPASAAAPCCVPALEPLPIVYVGRKPKVEQLSNMIVRSCKCS 407
DB 344 NOHNPASAAAPCCVPALEPLPIVYVGRKPKVEQLSNMIVRSCKCS 390

RESULT 5
US-07-669-171-2
; Sequence 2, Application US/07669171
; Patent No. 5304541
; GENERAL INFORMATION:
; APPLICANT: PURCHIO, ANTHONY F.
; APPLICANT: MADISEN, LINDA
; APPLICANT: MERWIN, JUNE RAE
; TITLE OF INVENTION: TGF-B1/D2: A NOVEL CHIMERIC TRANSFORMING
; TITLE OF INVENTION: GROWTH FACTOR-BETA
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 AVENUE OF THE AMERICAS
; CITY: NEW YORK
; STATE: N.Y.
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/669,171
; FILING DATE: 19910314
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MISROCK, S. LESLIE
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 5624-159-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 390 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-07-669-171-2

Query Match      88.7%; Score 1914.5; DB 1; Length 390;
Best Local Similarity 89.4%; Pred. No. 1.1e-168;
Matches 364; Conservative 10; Mismatches 16; Indels 17; Gaps 1;

QY 1 MAPSGRLRLPLLLPLWLLVLTGPPAAGLSTCKTIDMELVKKRKEAIRGOILSKRLA 60
DB 1 MPFSGRLRLPLLLPLWLLVLTGPPAAGLSTCKTIDMELVKKRKEAIRGOILSKRLA 60
QY 61 SPFSGQGVPPGGLPEAVLALYNSTRDRVAGESVEPEPEADYYAKEVTRVLMVETNEI 120
DB 61 SPFSGQGVPPGGLPEAVLALYNSTRDRVAGESVEPEPEADYYAKEVTRVLMVETNEI 120
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121	YDKFKQSTHSIYMFNTSELREAVPEPVLISRAELRLRLKLVKEQHVELYOKYSNNSWR	180
181	YLSNRLLPASDSEPWLSFSDVTGVVQWMLTRREIAEGFRLSAHSSDSOKNTLHVEINGFN	240
181	YLSNRLLPASNPSEWLSFSDVTGVVQWMLSRGGEIEGFRLSAHCSCDSKNTLQVDINGFT	240
241	SGRRGLATIIGHNRPFLLLMATPLERAQHLHSRRHRLDTHSYPDYDPDVYASLALDIN	300
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301	YCFSTSEKNCVROLYIDFRKDLGKWIHEPKGYHANFCLGPGCPYIWSLDTOYSKVLYLY	360
284	YCFSTSEKNCVROLYIDFRKDLGKWIHEPKGYHANFCLGPGCPYIWSLDTOYSKVLYLY	343
361	NOHNPGASAAACCVPQALEPLPIVYVYGRKPKVEQLSNMIVRSCKKS	407
344	NOHNPGASAAACCVPQALEPLPIVYVYGRKPKVEQLSNMIVRSCKKS	390

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Query Match 88.4%; Score 1909; DB 5; Length 394;
Best Local Similarity 89.5%; pred. NO. 3.5e-168;

```

Malches 365; Conservative 10; Mismatches 15; Indels 18; Gaps 2;
QY 1 MAPSGRLRLLPPLLWLLVLTGPRPAAGLSTCKTIIDMFLVKRKRIEAIKQILSKURLA 60
D 1 MPSPGLRLPLPLLWLLVLTGPPAAGLSTCKTIIDMLVKRKRIEAIKRGQILSKURLA 60
QY 61 SPSPSQGDVPGPPLPEAVLALYNSTRORVAGESVEPEPEADYYAKEVTIVLVAVESNQI 120
D 61 SPSPSQGEVPPGPPLPEAVLALYNSTRORVAGESAEPEPEADYYAKEVTIKVLAVETHNEI 120
QY 121 YDFKCTGPHSLYMLFNTSELREAVPPVLLSRAELRL--RLKLKVGHVELYKYKYSNDSW 179
D 121 YDFKQKSTHSIYWFNTSELREAVPEPVLLSRAELRLRLKLKVGHVELYKYKYSNSNW 180
QY 180 RYLSNRLAPSDSPENLSPDVTVGWQWLTRREAIGFRLSAHSSDSKDONTLHVELNGF 239
D 181 RYLSNRLAPSDSPENLSPDVTVGWQWLSRGGEEICFRLSAHSCDSRDRTIQVDINGF 240
QY 240 NSGRRGDLATIHGMNRPFLLMATPLERAQHLSHRRRALDINSYDYDPDYASLALDT 299
D 241 TTGRRGDLATIHGMNRPFLLMATPLERAQHLOSSRHRR-----ALDT 283
QY 300 NYCFSSTEKNCCVROLXYIDPKDLGHWKHIEHPKGXHYANFCLGPCPYTWSLDTOYSKVIAL 359
D 284 NYCFSSTEKNCCVROLXYIDFKDLGHWKHIEHPKGXHYANFCLGPCPYTWSLDTOYSKVIAL 343
QY 360 YNOHNPGASAAPCCVQALESPLPIVVYVGKPKVEQLSNMIVRSCKCS 407
D 344 YNOHNPGASAAPCCVQALESPLPIVVYVGKPKVEQLSNMIVRSCKCS 391

RESULT 7
US-08-132-405-3
: Sequence 3, Application US/08132405
: Patent No. 5409896
: GENERAL INFORMATION:
: APPLICANT: Ammann, Arthur J.
: INVENTOR: Rudman, Christopher G.
: TITLE OF INVENTION: Method of Inducing Bone Growth Using
: TITLE OF INVENTION: TGF-Beta
: NUMBER OF SEQUENCES: 5
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genentech, Inc.
: STREET: 460 Point San Bruno Blvd
: CITY: South San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94080
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: patin (Genentech)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/132,405
: FILING DATE: 06-OCT-1993
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/063841
: FILING DATE: 18-MAY-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/790856
: FILING DATE: 12-NOV-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/401906
: FILING DATE: 01-SEP-1989
: ATTORNEY/AGENT INFORMATION:
: NAME: Hasak, Janet E.
: REGISTRATION NUMBER: 28,616
: REFERENCE/DOCKET NUMBER: 597DLC2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415/225-1896
: TELEFAX: 415/952-9881

```

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; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 412 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-132-405-3

Query Match          38.4%; Score 828.5; DB 1; Length 412;
Best Local Similarity 44.5%; Pred. No. 2.6e-68;
Matches 189; Conservative 57; Mismatches 126; Indels 53; Gaps 13;

QY 15 LMLVLTGPRPAAGLSTCKTIDMELVKRKRIRAIHQILSKRLASPPSQGDVPPGPLP 74
Db 9 LVVALLNFATVLSLSLSTCTIDFGHIKKRVRVIRGQILSKRLTSPPEPTVMT--HVP 66

QY 75 EAVLALYNSTRORVA--GESVE---PEPEPEADYAKVTRVLMVE---SGNQIYDKFKG 126
Db 67 QVVALYNSTRRELLEEHGKERKEGCTQENTSEYAKETHKFMDIQGLAEHNELAVCPKG 126

QY 127 TPHSLYMLFNTSELRAVPEPVLLSRAELRLRL---KLKVEQHVLYQKYSND----S 178
Db 127 ITSKVFR-FNVSSVEK---NRTNLFRAEFRLVVPNPSSKRNEQRIELFQILRPDEHIAK 182

QY 179 WRYLSNRLLAPSDSPWLSFDVTGVVQWRLTRREALTEGFRLSAH-----SSSDSKDN- 230
Db 183 QRYIGCKNLPTRGTAEWLSFDVDTVREWLLRRESNLGLEISIHCPCHTFQPNGDILENI 242

QY 231 --TLHVEINGFNS---GRRGDLATIGHM---NRPFLLMATPLERAQHLHSSRRALDT 282
Db 243 HEYMEIKFKGVNDHGRGDLGRLLKQKDNPNPHILMMIPPHRLDNPQGGQGRK----S 298

QY 283 NSPYDVPDYASALADTNYCFSSSTEKNCCVROLYIDFRKDLGKWKIHEPKGYHANFCLGP 342
Db 343 CPYIWSLDTQYKVLALYNQHNPGASAPCCVQALEPLPIVYVGRKPKVEQLSNMIVR 402
Db 348 CPYLSADTTHSTVLGLYNTLNPEASAPCCVQDLEPLTILYVYVGRTPKVEQLSNMIVK 407

QY 403 SCKCS 407
Db 408 SCKCS 412

RESULT 8
US-08-395-939A-3
; Sequence 3, Application US/08395939A
; Patent No. 5604204
; GENERAL INFORMATION:
; APPLICANT: Ammann, Arthur J.
; APPLICANT: Rudman, Christopher G.
; TITLE OF INVENTION: TGF-BETA COMPOSITION FOR INDUCING BONE
; TITLE OF INVENTION: GROWTH
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 350 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/395,939A
; FILING DATE: 27-FEB-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/132405

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; FILING DATE: 12-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/063841
; FILING DATE: 18-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/790856
; FILING DATE: 12-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/401906
; FILING DATE: 1-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28 616
; REFERENCE/DOCKET NUMBER: P0597D1C2D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 412 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-395-939A-3

Query Match          38.4%; Score 828.5; DB 1; Length 412;
Best Local Similarity 44.5%; Pred. No. 2.6e-68;
Matches 189; Conservative 57; Mismatches 126; Indels 53; Gaps 13;

QY 15 LMLVLTGPRPAAGLSTCKTIDMELVKRKRIRAIHQILSKRLASPPSQGDVPPGPLP 74
Db 9 LVVALLNFATVLSLSLSTCTIDFGHIKKRVRVIRGQILSKRLTSPPEPTVMT--HVP 66

QY 75 EAVLALYNSTRORVA--GESVE---PEPEPEADYAKVTRVLMVE---SGNQIYDKFKG 126
Db 67 QVVALYNSTRRELLEEHGKERKEGCTQENTSEYAKETHKFMDIQGLAEHNELAVCPKG 126

QY 127 TPHSLYMLFNTSELRAVPEPVLLSRAELRLRL---KLKVEQHVLYQKYSND----S 178
Db 127 ITSKVFR-FNVSSVEK---NRTNLFRAEFRLVVPNPSSKRNEQRIELFQILRPDEHIAK 182

QY 179 WRYLSNRLLAPSDSPWLSFDVTGVVQWRLTRREALTEGFRLSAH-----SSSDSKDN- 230
Db 183 QRYIGCKNLPTRGTAEWLSFDVDTVREWLLRRESNLGLEISIHCPCHTFQPNGDILENI 242

QY 231 --TLHVEINGFNS---GRRGDLATIGHM---NRPFLLMATPLERAQHLHSSRRALDT 282
Db 243 HEYMEIKFKGVNDHGRGDLGRLLKQKDNPNPHILMMIPPHRLDNPQGGQGRK----S 298

QY 283 NSPYDVPDYASALADTNYCFSSSTEKNCCVROLYIDFRKDLGKWKIHEPKGYHANFCLGP 342
Db 299 -----KRALDNTYCFRNLENCVVRPLYIDFRQDLGKWKIHEPKGYANFCSGP 347

QY 343 CPYIWSLDTQYKVLALYNQHNPGASAPCCVQALEPLPIVYVGRKPKVEQLSNMIVR 402
Db 348 CPYLSADTTHSTVLGLYNTLNPEASAPCCVQDLEPLTILYVYVGRTPKVEQLSNMIVK 407

QY 403 SCKCS 407
Db 408 SCKCS 412

RESULT 9
US-09-380-662-21
; Sequence 21, Application US/09380662
; Patent No. 6376199
; GENERAL INFORMATION:
; APPLICANT: Caniggia, Isabella
; APPLICANT: Post, Martin
; APPLICANT: Lye, Stephen
; TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF TROPHOBLAST
; FILE REFERENCE: 11757.39USNO
; CURRENT APPLICATION NUMBER: US/09/380,662

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; CURRENT FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: PCT/CA98/00180
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: US 60/039,919
; PRIOR FILING DATE: 1997-03-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent version 3.0
; SEQ ID NO 21
; LENGTH: 412
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-380-662-21

Query Match      38.2%; Score 824.5; DB 4; Length 412;
Best Local Similarity 44.2%; Pred. No. 6.1e-68;
Matches 188; Conservative 58; Mismatches 126; Indels 53; Gaps 13;

QY 15 LMLVLTPGPPAAGLSTCKTIDMLVKKRIEARGQILSKRLASPPSGDVPPLP 74
Db 9 LVLALLNFATVSLSTCTTDFGHKKRVEAIRGQILSKRLTSPPEPTVMT--HVP 66
QY 75 EAVLYNSTR---DRVAGESVE--PEPEADYYAKEVTRVLAVE---SGNQIYDKFKG 126
Db 67 QVLYALYNSTRLEEMHGEREGCTQENTSEYYAKEIHKFDMIOGLAEHNELAVCPKG 126
QY 127 TPHSLYMLNTPSELRAVPEPVLSSRAELRLRL---KLKVEQHVLYQKYSND----S 178
Db 127 ITSQVFR-FNVSSVEK---NRTNLFRAFRVLRVNPSPSKRNEQRIELFQILRPDEHIAK 182
QY 179 WRYLNRLLAPSDSPWLSDFTGVVYQWLTRREAIEGFRLSAH-----SSDSKDN- 230
Db 183 QRVIGKGNLPTRTAGLWLSFQVDTVREWLLRRSNLGLSIRHCPCHTFQPGDILENI 242
QY 231 --TLHVEINGFNS---GRRGLATIGHM---NRPLLMLATPLERAQHLHSSRRALDT 282
Db 243 HEVMEIKFGVDNEDDHGRDLGRKKQKDHHPHLLMLNIPPHRLDNPQGGQGRK---- 298
QY 283 NSYPYDVPDYASIALDTNYCFSSSTEKNCCVROLYIDFRKDLGKWKIHPKGYHANFCLGP 342
Db 343 CPYIWSLDTQYKVLALYNQHNPGASAPCCVPQALEPLPIVYVYGRKPKVEQLSNMIVR 402
QY 348 CPYLSADTTHSTVGLYNTLNPEASAPCCVPQDLEPLTILYVYGRTPKVEQLSNMIVK 407
Db 403 SKCS 407
Db 408 SKCS 412

RESULT 10
PCT-US91-04541-2
; Sequence 2, Application PC/TUS9104541
; GENERAL INFORMATION:
; APPLICANT: Oncogene Science Inc.
; TITLE OF INVENTION: TISSUE DERIVED TUMOR GROWTH INHIBITORS
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/04541
; FILING DATE: 19910625
; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 1919/22669-F-PCI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)977-9550
; TELEFAX: (212)664-0525
; TELEX: 422523 COOP U1
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 412 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US91-04541-2

Query Match      38.2%; Score 824.5; DB 5; Length 412;
Best Local Similarity 44.2%; Pred. No. 6.1e-68;
Matches 188; Conservative 58; Mismatches 126; Indels 53; Gaps 13;

QY 15 LMLVLTPGPPAAGLSTCKTIDMLVKKRIEARGQILSKRLASPPSGDVPPLP 74
Db 9 LVLALLNFATVSLSTCTTDFGHKKRVEAIRGQILSKRLTSPPEPTVMT--HVP 66
QY 75 EAVLYNSTR---DRVAGESVE--PEPEADYYAKEVTRVLAVE---SGNQIYDKFKG 126
Db 67 QVLYALYNSTRLEEMHGEREGCTQENTSEYYAKEIHKFDMIOGLAEHNELAVCPKG 126
QY 127 TPHSLYMLNTPSELRAVPEPVLSSRAELRLRL---KLKVEQHVLYQKYSND----S 178
Db 127 ITSQVFR-FNVSSVEK---NRTNLFRAFRVLRVNPSPSKRNEQRIELFQILRPDEHIAK 182
QY 179 WRYLNRLLAPSDSPWLSDFTGVVYQWLTRREAIEGFRLSAH-----SSDSKDN- 230
Db 183 QRVIGKGNLPTRTAGLWLSFQVDTVREWLLRRSNLGLSIRHCPCHTFQPGDILENI 242
QY 231 --TLHVEINGFNS---GRRGLATIGHM---NRPLLMLATPLERAQHLHSSRRALDT 282
Db 243 HEVMEIKFGVDNEDDHGRDLGRKKQKDHHPHLLMLNIPPHRLDNPQGGQGRK---- 298
QY 283 NSYPYDVPDYASIALDTNYCFSSSTEKNCCVROLYIDFRKDLGKWKIHPKGYHANFCLGP 342
Db 343 CPYIWSLDTQYKVLALYNQHNPGASAPCCVPQALEPLPIVYVYGRKPKVEQLSNMIVR 402
QY 348 CPYLSADTTHSTVGLYNTLNPEASAPCCVPQDLEPLTILYVYGRTPKVEQLSNMIVK 407
Db 403 SKCS 407
Db 408 SKCS 412

RESULT 11
5262319-2
; Patent No. 5262319
; APPLICANT: IWATA, KENNETH K.; FOULKES, J. GORDON; DIJKE,
; PETER T.; HALEY, JOHN D.
; TITLE OF INVENTION: METHOD FOR OBTAINING BONE MARROW FREE
; OF TUMOR CELLS USING TRANSFORMING GROWTH FACTOR B3
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/543,341
; FILING DATE: 25-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 353,410
; FILING DATE: 17-MAY-1989
; APPLICATION NUMBER: 183,410
; FILING DATE: 20-APR-1988
; APPLICATION NUMBER: 111,022
; FILING DATE: 20-OCT-1987
; APPLICATION NUMBER: 922,121
; FILING DATE: 20-OCT-1986
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; APPLICATION NUMBER: 847,931
; FILING DATE: 07-APR-1986
; APPLICATION NUMBER: 725,003
; FILING DATE: 19-APR-1985
; SEQ ID NO:2
; LENGTH: 412
5262319-2

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Query Match      38.2%; Score 824.5; DB 6; Length 412;
Best Local Similarity 44.2%; Pred. No. 6.1e-66;
Matches 188; Conservative 58; Mismatches 126; Indels 53; Gaps 13;

QY 15 LMLLVTPGPAAGLSTCKTIDMELVKRKRIEAIKQILSKRLASPPSGQGVPPGCLP 74
Db 9 LVVALLNFATVSLSTCTTDFGHKKRKRVEAIRGQILSKRLTSPPEPTVMT--HVP 66
QY 75 EAVLALYNSTR--DRVAGESVE--PEPEADYAKVIRVLMVE---SGNOIYDKFKG 126
Db 67 YQVLALYNSTRLEENHGEREGCTOENTSEYAYAKEIHKFDMIOGLAEHNELAVCPKG 126
QY 127 TPHSLYMLFNTSELREAVPEPVLLSRAELRLRL----KLKVEQHVELYQKYSND----S 178
Db 127 ITSQVFR-FNVSSVEK---NRTNLFRAEFRLVNPSPSSKNEQRIELFOILRPDEHIAK 182
QY 179 WRYLSNRLAPSDSPWLSFDVTGVVROWLTRREAIEGFRLSAH-----SSSDSKDN- 230
Db 183 QRYIGGKNLPTGTAEWLSFDVDTVREMLLRRESNLGLEISIHCPCHTFQPNGDILENI 242
QY 231 --TLHVEINGFNS---GRGDLATIHGM---NRPFLLLMATPLERAQHLHSSRRRALDT 282
Db 243 HEVMEIKFGVDNEHDHGRDGLRLKQKQDHNPHLILMIPPHRLONPGQGGQK---- 298
QY 283 NSYPVDPDYASLADTNYCFSSSTEKNCCVRLYIDFRKDLGKWKIHEPKGYHANFCLGP 342
Db 299 -----KRALDINFCRNLEENCCVRLYIDFRQDLGKWKIHEPKGYHANFCSGP 347
QY 343 CPYIWSLDTQYSKVLALYNQHNFCASAPCCVPOALEPLTVYVGRKPKVEQLSNMIVR 402
Db 348 CPYLSADTTHSTVLGLYNTLNPEASAPCCVPODLEPLTILYVGRTPKVEQLSNMVK 407
QY 403 SKCS 407
Db 408 SKCS 412

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RESULT 12
PCT-US91-01861-3
; Sequence 3, Application PC/TUS9101861
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Method of Pre-disposing Mammals to
; TITLE OF INVENTION: Accelerated Tissue Repair
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/01861
; FILING DATE: 19910320
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Ser. No. 07/504,495
; FILING DATE: 4 April 1990
; ATTORNEY/AGENT INFORMATION:

```

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; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 637
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/266-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 410 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
PCT-US91-01861-3

Query Match      38.1%; Score 823.5; DB 5; Length 410;
Best Local Similarity 44.2%; Pred. No. 7.5e-66;
Matches 188; Conservative 58; Mismatches 126; Indels 53; Gaps 13;

QY 15 LMLLVTPGPAAGLSTCKTIDMELVKRKRIEAIKQILSKRLASPPSGQGVPPGCLP 74
Db 7 LVVALLNFATVSLSTCTTDFGHKKRKRVEAIRGQILSKRLTSPPEPTVMT--HVP 64
QY 75 EAVLALYNSTRDVA--GESVE--PEPEADYAKVIRVLMVE---SGNOIYDKFKG 126
Db 65 YQVLALYNSTRLEENHGEREGCTOENTSEYAYAKEIHKFDMIOGLAEHNELAVCPKG 124
QY 127 TPHSLYMLFNTSELREAVPEPVLLSRAELRLRL----KLKVEQHVELYQKYSND----S 178
Db 125 ITSQVFR-FNVSSVEK---NRTNLFRAEFRLVNPSPSSKNEQRIELFOILRPDEHIAK 180
QY 179 WRYLSNRLAPSDSPWLSFDVTGVVROWLTRREAIEGFRLSAH-----SSSDSKDN- 230
Db 181 QRYIGGKNLPTGTAEWLSFDVDTVREMLLRRESNLGLEISIHCPCHTFQPNGDILENI 240
QY 231 --TLHVEINGFNS---GRGDLATIHGM---NRPFLLLMATPLERAQHLHSSRRRALDT 282
Db 241 HEVMEIKFGVDNEHDHGRDGLRLKQKQDHNPHLILMIPPHRLONPGQGGQK---- 296
QY 283 NSYPVDPDYASLADTNYCFSSSTEKNCCVRLYIDFRKDLGKWKIHEPKGYHANFCLGP 342
Db 297 -----KRALDINFCRNLEENCCVRLYIDFRQDLGKWKIHEPKGYHANFCSGP 345
QY 343 CPYIWSLDTQYSKVLALYNQHNFCASAPCCVPOALEPLTVYVGRKPKVEQLSNMIVR 402
Db 346 CPYLSADTTHSTVLGLYNTLNPEASAPCCVPODLEPLTILYVGRTPKVEQLSNMVK 405
QY 403 SKCS 407
Db 406 SKCS 410

RESULT 13
US-08-132-405-2
; Sequence 2, Application US/08132405
; Patent No. 5409896
; GENERAL INFORMATION:
; APPLICANT: Ammann, Arthur J.
; APPLICANT: Rudmann, Christopher G.
; TITLE OF INVENTION: Method of Inducing Bone Growth Using
; TITLE OF INVENTION: TGF-Beta
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)

```

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/132,405
; FILING DATE: 06-OCT-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/063841
; FILING DATE: 18-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/790856
; FILING DATE: 12-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/401906
; FILING DATE: 01-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REFERENCE/DOCKET NUMBER: 597D1C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 414 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
US-08-132-405-2

Query Match 37.5%; Score 809; DB 1; Length 414;
Best Local Similarity 43.2%; Pred. No. 1.7e-66;
Matches 181; Conservative 62; Mismatches 116; Indels 60; Gaps 14;

QY 27 AAGLSTCTIDMELVKRRIRIARQILSKLRASPPSQGDVP--PGPLPAVLALYNSTR 85
DB 18 ALSLSTCTLDQFMRRRIEIRQILSKLRASPPSQGDVP--DYPEPEVPEVISIYNSTR 75

QY 86 D-----RVAGESVEPEPE--PEADYIAKEVTRVLM---VESGNQIYDKFGTSPHSLYMLFNT 137
DB 76 DLLQEKASRAAACERERSDEEYIAKEVYKIDMPFPFSENALPPTFY-RPYFRIVRFDV 134

QY 138 SELREAVPEPVLLSRAELRLRL---KLKV-EQHVELYQ-----KYSNDSWRVLSNRLLA 188
DB 135 SAMEKNASN---LVKAERFVRLQNPVKARVPEQRIELYQLKSKDLTSPRTQRYIDSKVVK 191

QY 189 PSDSPEWLSFDVTGVVROWLITRREALFGFRLSAHSSS-----DSKDNLTLMHVE-- 235
DB 192 TRAEGEWLSFDVTDVAVHEWLHKDRNLGFKLSLHCPCTTFVPSNNYIIPNKSELEARFA 251

QY 236 -INGFNSGRRGLDGLATIHGMNR-----PFLLLMATPLERAQHLHSRRRALDNTNSPYD 288
DB 252 GIDGTSTVTSQDKTIKSTRKNSGKTPTLHLLMLPSYRLSQQTNRRKKR----- 302

QY 289 VPDYASLALDNTNYCFSTEKNCCVRLYIDFRKDLGKWKIHEPKGYHANFCLGCPYIWS 348
DB 303 -----ALDAAYCFRNQVQNCCLRPYIDFRKDLGKWKIHEPKGYNANFCAGACPYLWS 355

QY 349 LDTQYSKVLALYNQHNPCASAPCCVPOALEPLPIVTVYVGHKPKVQOLSNNIVRSCKCS 407
DB 356 SDTQHSRVLSLYNTINPEASAPCCVQDLEPLTILYIYIGTKPIEQLSNNIVRSCKCS 414

RESULT 14
US-08-395-939A-2
; Sequence 2, Application US/08394939A
; Patent No. 5604204
; GENERAL INFORMATION:
; APPLICANT: Ammann, Arthur J.
; APPLICANT: Rudman, Christopher G.
; TITLE OF INVENTION: TGF-BETA COMPOSITION FOR INDUCING BONE
; TITLE OF INVENTION: GROWTH
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.

```

```

; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/395,939A
; FILING DATE: 27-FEB-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/132405
; FILING DATE: 12-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/063841
; FILING DATE: 18-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/790856
; FILING DATE: 12-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/401906
; FILING DATE: 1-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: P0597D1C2D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 414 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
;
US-08-395-939A-2

Query Match 37.5%; Score 809; DB 1; Length 414;
Best Local Similarity 43.2%; Pred. No. 1.7e-66;
Matches 181; Conservative 62; Mismatches 116; Indels 60; Gaps 14;

QY 27 AAGLSTCTIDMELVKRRIRIARQILSKLRASPPSQGDVP--PGPLPAVLALYNSTR 85
DB 18 ALSLSTCTLDQFMRRRIEIRQILSKLRASPPSQGDVP--DYPEPEVPEVISIYNSTR 75

QY 86 D-----RVAGESVEPEPE--PEADYIAKEVTRVLM---VESGNQIYDKFGTSPHSLYMLFNT 137
DB 76 DLLQEKASRAAACERERSDEEYIAKEVYKIDMPFPFSENALPPTFY-RPYFRIVRFDV 134

QY 138 SELREAVPEPVLLSRAELRLRL---KLKV-EQHVELYQ-----KYSNDSWRVLSNRLLA 188
DB 135 SAMEKNASN---LVKAERFVRLQNPVKARVPEQRIELYQLKSKDLTSPRTQRYIDSKVVK 191

QY 189 PSDSPEWLSFDVTGVVROWLITRREALFGFRLSAHSSS-----DSKDNLTLMHVE-- 235
DB 192 TRAEGEWLSFDVTDVAVHEWLHKDRNLGFKLSLHCPCTTFVPSNNYIIPNKSELEARFA 251

QY 236 -INGFNSGRRGLDGLATIHGMNR-----PFLLLMATPLERAQHLHSRRRALDNTNSPYD 288
DB 252 GIDGTSTVTSQDKTIKSTRKNSGKTPTLHLLMLPSYRLSQQTNRRKKR----- 302

QY 289 VPDYASLALDNTNYCFSTEKNCCVRLYIDFRKDLGKWKIHEPKGYHANFCLGCPYIWS 348
DB 303 -----ALDAAYCFRNQVQNCCLRPYIDFRKDLGKWKIHEPKGYNANFCAGACPYLWS 355

QY 349 LDTQYSKVLALYNQHNPCASAPCCVPOALEPLPIVTVYVGHKPKVQOLSNNIVRSCKCS 407
DB 356 SDTQHSRVLSLYNTINPEASAPCCVQDLEPLTILYIYIGTKPIEQLSNNIVRSCKCS 414

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.
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Run on: October 7, 2003, 18:04:22 ; Search time 67 seconds
(without alignments)
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 587654 seqs, 15812981 residues
Total number of hits satisfying chosen parameters: 587654
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pcp:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pcp:*
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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pcp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2030.5	94.0	390	11	US-09-214-592-26
2	1929.5	89.4	390	11	US-09-214-592-29
3	1926.5	89.2	390	15	US-10-087-268-2
4	1919.5	88.9	390	15	US-10-087-268-5
5	1916.5	88.8	390	12	US-10-276-947-1
6	1914.5	88.7	390	11	US-09-214-592-33
7	1909	88.4	391	11	US-09-214-592-17
8	1905.5	88.3	390	10	US-09-756-283A-23
9	1893.5	87.0	390	11	US-09-214-592-28
10	1835.5	85.0	390	11	US-09-214-592-20
11	1835.5	85.0	390	11	US-09-214-592-23
12	1572.5	72.8	315	11	US-09-214-592-25
13	1262.5	58.5	455	10	US-09-756-283A-20
14	1139	52.8	447	10	US-09-756-283A-22
15	1047	48.5	373	11	US-09-214-592-32

16	871.5	40.4	412	11	US-09-214-592-31	Sequence 31, Appl
17	868.5	40.2	382	11	US-09-214-592-34	Sequence 34, Appl
18	868	40.2	383	10	US-09-756-283A-27	Sequence 27, Appl
19	834	38.6	409	11	US-09-214-592-27	Sequence 27, Appl
20	827.5	38.3	410	11	US-09-214-592-22	Sequence 22, Appl
21	826.5	38.3	412	11	US-09-214-592-24	Sequence 24, Appl
22	824.5	38.2	412	11	US-09-214-592-19	Sequence 19, Appl
23	824.5	38.2	412	11	US-10-028-156-21	Sequence 21, Appl
24	824	38.2	414	11	US-09-214-592-21	Sequence 21, Appl
25	820.5	38.0	412	10	US-09-756-283A-25	Sequence 25, Appl
26	809	37.5	414	10	US-09-756-283A-24	Sequence 24, Appl
27	809	37.5	414	11	US-09-214-592-18	Sequence 18, Appl
28	808	37.4	412	11	US-09-214-592-30	Sequence 30, Appl
29	792	36.7	304	10	US-09-756-283A-26	Sequence 26, Appl
30	753.5	34.9	139	14	US-10-002-278-8	Sequence 8, Appl
31	638	29.6	112	10	US-09-813-271B-2	Sequence 2, Appl
32	638	29.6	113	10	US-09-813-398-13	Sequence 13, Appl
33	638	29.6	114	10	US-09-813-459-22	Sequence 22, Appl
34	638	29.6	114	14	US-10-115-406-21	Sequence 21, Appl
35	638	29.6	114	15	US-10-154-333-23	Sequence 23, Appl
36	638	29.6	115	10	US-09-859-211-47	Sequence 47, Appl
37	638	29.6	115	10	US-09-880-708-25	Sequence 25, Appl
38	638	29.6	115	11	US-09-872-856-47	Sequence 47, Appl
39	638	29.6	115	15	US-10-335-483-29	Sequence 29, Appl
40	562	26.0	98	2	US-10-187-394-1	Sequence 1, Appl
41	542	25.1	116	14	US-10-115-406-24	Sequence 24, Appl
42	542	25.1	116	15	US-10-154-333-26	Sequence 26, Appl
43	535	24.9	112	10	US-09-813-271B-8	Sequence 8, Appl
44	504	23.3	112	10	US-09-813-271B-12	Sequence 12, Appl
45	504	23.3	114	14	US-10-115-406-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-09-214-592-26
; Sequence 26, Application US/09214592A
; Publication No. US20030027218A1
; GENERAL INFORMATION:
; APPLICANT: Yamasaki,CMotoo
; APPLICANT: Shibata,Ckenjl
; APPLICANT: Sato,Cyasufumi
; TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIATION OF LATENT TGF- AND METHOD
; FILE REFERENCE: 11060
; CURRENT APPLICATION NUMBER: US/09/214,592A
; CURRENT FILING DATE: 1999-01-18
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE:
; SEQ ID NO 26
; LENGTH: 390
; TYPE: PRT
; ORGANISM: porcine
; US-09-214-592-26

Query Match	94.0%	Score 2030.5;	DB 11;	Length 390;
Best Local Similarity	94.8%	Pred. No. 3.9e+180;		
Matches 386;	Conservative 1;	Mismatches 3;	Indels 17;	Gaps 1;
Qy	1	MAPSGURLPLLLPLLLVLTGPRPAAGLSTCKTIDMELVKKRIEAIIRGQILSKRLA	60	
Db	1	MPFSGRLPLLLPLLLVLTGPRPAAGLSTCKTIDMELVKKRIEAIIRGQILSKRLA	60	
Qy	61	SPFSGQDVPGPPLPEAVLALYNSTRVAGESVEPEPEADYYAKEVTRVLMVESGNI	120	
Db	61	SPFSGQDVPGPPLPEAVLALYNSTRVAGESVEPEPEADYYAKEVTRVLMVESGNI	120	
Qy	121	YDKFKGTGPHSLYMLFNTSELREAVPEVLLLSRAELRLRLKLVKVEOHVLYQKYSNDSWR	180	
Db	121	YDKFKGTGPHSLYMLFNTSELREAVPEVLLLSRAELRLRLKLVKVEOHVLYQKYSNDSWR	180	
Qy	181	YLSNRLAPSDSPWLSFDVTGVVRQWLTRRAIEGFRLSAHSSSDKNTLHVINGFN	240	

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Db 181 YLSNRLAPSDPEWLSFDVTGVVQWLTREAEIGFRLSAHSCDSKDNTHLVEINGFN 240
QY 241 SGRGDLATIHGMNRPFLMLMATPLERAQHLHSSRRRALDNTNSYPDVPDYASALDTN 300
Db 241 SGRGDLATIHGMNRPFLMLMATPLERAQHLHSSRRRALDNTNSYPDVPDYASALDTN 283
QY 301 YCFSTKNCVQRLYIDFKDLGKWKIHEPKGYHANFCLGCPYIWSLDTQYSKVLALY 360
Db 284 YCFSTKNCVQRLYIDFKDLGKWKIHEPKGYHANFCLGCPYIWSLDTQYSKVLALY 343
QY 361 NOHNPASAPCCVQPALEPLPIVYVGRKPKVEQLSNMIVRSCKCS 407
Db 344 NOHNPASAPCCVQPALEPLPIVYVGRKPKVEQLSNMIVRSCKCS 390

RESULT 2
US-09-214-592-29
; Sequence 29, Application US/09214592A
; Publication No. US20030027218A1
; GENERAL INFORMATION:
; APPLICANT: Yamasaki, Chotao
; APPLICANT: Shibata, Kenji
; APPLICANT: Sato, Chisafumi
; TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND METHOD
; TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS
; FILE REFERENCE: 11060
; CURRENT APPLICATION NUMBER: US/09/214,592A
; CURRENT FILING DATE: 1999-01-18
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE:
; SEQ ID NO 29
; LENGTH: 390
; TYPE: PRT
; ORGANISM: ovine
US-09-214-592-29
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Query Match 89.4%; Score 1929.5; DB 11; Length 390;
Best Local Similarity 89.7%; Pred. No. 9.4e-171;
Matches 365; Conservative 10; Mismatches 15; Indels 17; Gaps 1;

QY 1 MAPSGLRLPLLLPLLLVLTGPRPAAGLSTCKTIDMELVKKRIEAIKQILSKRLA 60
Db 1 MPPSGLRLPLLLPLLLVLTGPRPAAGLSTCKTIDMELVKKRIEAIKQILSKRLA 60
QY 61 SPPSQGDVPPGPLEAVLALYNSTRDVAGESVEPEPEADYAKETVRLMWESNQI 120
Db 61 SPPSQGDVPPGPLEAVLALYNSTRDVAGESAEPEPEADYAKETVRLMWVEIGNI 120
QY 121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLRLKLVQEHVELYQKYSNDSWR 180
Db 121 YDKMKSSHSIYMFNTSELREAVPEPVLLSRADVRLRLKLVQEHVELYQKYSNNSWR 180
QY 181 YLSNRLAPSDPEWLSFDVTGVVQWLTREAEIGFRLSAHSSDSKDNTHLVEINGFN 240
Db 181 YLSNRLAPSDPEWLSFDVTGVVQWLTREAEIGFRLSAHSCDSKDNTHLVDINGFT 240
QY 241 SGRGDLATIHGMNRPFLMLMATPLERAQHLHSSRRRALDNTNSYPDVPDYASALDTN 300
Db 241 SGRGDLATIHGMNRPFLMLMATPLERAQHLHSSRRRALDNTNSYPDVPDYASALDTN 283
QY 301 YCFSTKNCVQRLYIDFKDLGKWKIHEPKGYHANFCLGCPYIWSLDTQYSKVLALY 360
Db 284 YCFSTKNCVQRLYIDFKDLGKWKIHEPKGYHANFCLGCPYIWSLDTQYSKVLALY 343
QY 361 NOHNPASAPCCVQPALEPLPIVYVGRKPKVEQLSNMIVRSCKCS 407
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RESULT 3
US-10-087-268-2
; Sequence 2, Application US/10087268
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; Publication No. US20030119010A1
; GENERAL INFORMATION:
; APPLICANT: Jonsson, Julie Ruth
; APPLICANT: Powell, Elizabeth Ellen
; TITLE OF INVENTION: Polypeptides and polynucleotides linked to a disease or condit
; FILE REFERENCE: Fibrosis
; CURRENT APPLICATION NUMBER: US/10/087,268
; CURRENT FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Human
US-10-087-268-2
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Query Match 89.2%; Score 1926.5; DB 15; Length 390;
Best Local Similarity 89.9%; Pred. No. 1.8e-170;
Matches 366; Conservative 10; Mismatches 14; Indels 17; Gaps 1;

QY 1 MAPSGLRLPLLLPLLLVLTGPRPAAGLSTCKTIDMELVKKRIEAIKQILSKRLA 60
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Db 61 SPPSQGDVPPGPLEAVLALYNSTRDVAGESAEPEPEADYAKETVRLMWETHNEI 120
QY 121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLRLKLVQEHVELYQKYSNDSWR 180
Db 121 YDKFKQSTHSIYMFNTSELREAVPEPVLLSRAELRLRLKLVQEHVELYQKYSNNSWR 180
QY 181 YLSNRLAPSDPEWLSFDVTGVVQWLTREAEIGFRLSAHSSDSKDNTHLVEINGFN 240
Db 181 YLSNRLAPSDPEWLSFDVTGVVQWLSRGEIEGFLSAHSCDSRDNTHLQVDINGFT 240
QY 241 SGRGDLATIHGMNRPFLMLMATPLERAQHLHSSRRRALDNTNSYPDVPDYASALDTN 300
Db 241 TCRGDLATIHGMNRPFLMLMATPLERAQHLQSSRRRR-----ALDTN 283
QY 301 YCFSTKNCVQRLYIDFKDLGKWKIHEPKGYHANFCLGCPYIWSLDTQYSKVLALY 360
Db 284 YCFSTKNCVQRLYIDFKDLGKWKIHEPKGYHANFCLGCPYIWSLDTQYSKVLALY 343
QY 361 NOHNPASAPCCVQPALEPLPIVYVGRKPKVEQLSNMIVRSCKCS 407
Db 344 NOHNPASAPCCVQPALEPLPIVYVGRKPKVEQLSNMIVRSCKCS 390
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RESULT 4
US-10-087-268-5
; Sequence 5, Application US/10087268
; Publication No. US20030119010A1
; GENERAL INFORMATION:
; APPLICANT: Jonsson, Julie Ruth
; APPLICANT: Powell, Elizabeth Ellen
; TITLE OF INVENTION: Polypeptides and polynucleotides linked to a disease or condit
; FILE REFERENCE: Fibrosis
; CURRENT APPLICATION NUMBER: US/10/087,268
; CURRENT FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Human
US-10-087-268-5
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Query Match 88.9%; Score 1919.5; DB 15; Length 390;
Best Local Similarity 89.7%; Pred. No. 8e-170;
Matches 365; Conservative 10; Mismatches 15; Indels 17; Gaps 1;

QY 1 MAPSGLRLPLLLPLLLVLTGPRPAAGLSTCKTIDMELVKKRIEAIKQILSKRLA 60
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Db 1 MPPSGRLRLPLLLPLLLVLTGPPAAGLSTCKTIDMELVKRRIRIAIRGOILSKRLA 60
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Db 61 SPSSQGVPPGPPLEPAVLALYNSTRDRVAGESABPEPEADYAKVETRVLMVETHNEI 120
Qy 121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRALRLRLKLKVEQHVELYQKYSNDSWR 180
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Qy 181 YLSNRLAPSDEPWLSTFVTVGVVROWLTREAELEGFRLSAHSSDSKONTLHVEINGFN 240
Db 181 YLSNRLAPSDEPWLSTFVTVGVVROWLSRGGELEGFRLSAHSCSDSDNTLQVDINGFT 240
Qy 241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRRRALDNTNSYPDYDYLASLADTN 300
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Qy 301 YCFSTEKNCCVROLYIDFRKDLGKWKIHEPKGYHANFCLGPGCPYIWSLDTQYSKVLALY 360
Db 284 YCFSTEKNCCVROLYIDFRKDLGKWKIHEPKGYHANFCLGPGCPYIWSLDTQYSKVLALY 343
Qy 361 NOHNPASAAAPCCVQALPEPLPIVYVGRKPKVQQLSNMIVRSCKCS 407
Db 344 NOHNPASAAAPCCVQALPEPLPIVYVGRKPKVQQLSNMIVRSCKCS 390

RESULT 5

US-10-276-947-1
; Sequence 1, Application US/10276947
; Publication No. US20030176315A1
; GENERAL INFORMATION:
; APPLICANT: GLAXO GROUP LIMITED
; TITLE OF INVENTION: MEDICAL PRODUCTS
; FILE REFERENCE: PG3949
; CURRENT APPLICATION NUMBER: US/10/276.947
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: GB 0012991.6
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 0100286.4
; PRIOR FILING DATE: 2001-01-05
; SOFTWARE: Patent In Ver. 2.0
; NUMBER OF SEQ ID NOS: 1
; SEQ ID NO 1
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-276-947-1

Query Match 88.8%; Score 1916.5; DB 12; Length 390;
Best Local Similarity 89.7%; Pred. No. 1.5e-169;
Matches 365; Conservative 10; Mismatches 15; Indels 17; Gaps 1;
Qy 1 MAPSGRLRLPLLLPLLLVLTGPPAAGLSTCKTIDMELVKRRIRIAIRGOILSKRLA 60
Db 1 MPPSGRLRLPLLLPLLLVLTGPPAAGLSTCKTIDMELVKRRIRIAIRGOILSKRLA 60
Qy 61 SPSSQGVPPGPPLEPAVLALYNSTRDRVAGESVEPEPEADYAKVETRVLMVESGNOI 120
Db 61 SPSSQGVPPGPPLEPAVLALYNSTRDRVAGESAEPEPEADYAKVETRVLMVETHNEI 120
Qy 121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRALRLRLKLKVEQHVELYQKYSNDSWR 180
Db 121 YDKFKQSTHSIYMFNTSELREAVPEPVLLSRALRLRLKLKVEQHVELYQKYSNDSWR 180
Qy 181 YLSNRLAPSDEPWLSTFVTVGVVROWLTREAELEGFRLSAHSSDSKONTLHVEINGFN 240
Db 181 YLSNRLAPSDEPWLSTFVTVGVVROWLSRGGELEGFRLSAHSCSDSDNTLQVDINGFT 240
Qy 241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRRRALDNTNSYPDYDYLASLADTN 300
Db 241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRRHR-----ALDTN 283

Qy 301 YCFSTEKNCCVROLYIDFRKDLGKWKIHEPKGYHANFCLGPGCPYIWSLDTQYSKVLALY 360
Db 284 YCFSTEKNCCVROLYIDFRKDLGKWKIHEPKGYHANFCLGPGCPYIWSLDTQYSKVLALY 343
Qy 361 NOHNPASAAAPCCVQALPEPLPIVYVGRKPKVQQLSNMIVRSCKCS 407
Db 344 NOHNPASAAAPCCVQALPEPLPIVYVGRKPKVQQLSNMIVRSCKCS 390

RESULT 6

US-09-214-592-33
; Sequence 33, Application US/09214592A
; Publication No. US20030027218A1
; GENERAL INFORMATION:
; APPLICANT: Yamasaki, Cmotoo
; APPLICANT: Shibata, Ckenji
; APPLICANT: Sato, Cyasufumi
; TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND METHOD
; FILE REFERENCE: 11060
; CURRENT APPLICATION NUMBER: US/09/214.592A
; CURRENT FILING DATE: 1999-01-18
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE:
; SEQ ID NO 33
; LENGTH: 390
; TYPE: PRT
; ORGANISM: simian
US-09-214-592-33

Query Match 88.7%; Score 1914.5; DB 11; Length 390;
Best Local Similarity 89.4%; Pred. No. 2.3e-169;
Matches 364; Conservative 10; Mismatches 16; Indels 17; Gaps 1;
Qy 1 MAPSGRLRLPLLLPLLLVLTGPPAAGLSTCKTIDMELVKRRIRIAIRGOILSKRLA 60
Db 1 MPPSGRLRLPLLLPLLLVLTGPPAAGLSTCKTIDMELVKRRIRIAIRGOILSKRLA 60
Qy 61 SPSSQGVPPGPPLEPAVLALYNSTRDRVAGESVEPEPEADYAKVETRVLMVESGNOI 120
Db 61 SPSSQGVPPGPPLEPAVLALYNSTRDRVAGESAEPEPEADYAKVETRVLMVETHNEI 120
Qy 121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRALRLRLKLKVEQHVELYQKYSNDSWR 180
Db 121 YDKFKQSTHSIYMFNTSELREAVPEPVLLSRALRLRLKLKVEQHVELYQKYSNDSWR 180
Qy 181 YLSNRLAPSDEPWLSTFVTVGVVROWLTREAELEGFRLSAHSSDSKONTLHVEINGFN 240
Db 181 YLSNRLAPSDEPWLSTFVTVGVVROWLSRGGELEGFRLSAHSCSDSDNTLQVDINGFT 240
Qy 241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRRRALDNTNSYPDYDYLASLADTN 300
Db 241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRRHR-----ALDTN 283

Qy 301 YCFSTEKNCCVROLYIDFRKDLGKWKIHEPKGYHANFCLGPGCPYIWSLDTQYSKVLALY 360
Db 284 YCFSTEKNCCVROLYIDFRKDLGKWKIHEPKGYHANFCLGPGCPYIWSLDTQYSKVLALY 343
Qy 361 NOHNPASAAAPCCVQALPEPLPIVYVGRKPKVQQLSNMIVRSCKCS 407
Db 344 NOHNPASAAAPCCVQALPEPLPIVYVGRKPKVQQLSNMIVRSCKCS 390

RESULT 7

US-09-214-592-17
; Sequence 17, Application US/09214592A
; Publication No. US20030027218A1
; GENERAL INFORMATION:
; APPLICANT: Yamasaki, Cmotoo
; APPLICANT: Shibata, Ckenji
; APPLICANT: Sato, Cyasufumi
; TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND METHOD


```
; TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS
; FILE REFERENCE: 11060
; CURRENT APPLICATION NUMBER: US/09/214,592A
; CURRENT FILING DATE: 1999-01-1E
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE:
; SEQ ID NO 17
; LENGTH: 391
; TYPE: PRT
; ORGANISM: human
US-09-214-592-17

Query Match      88.4%; Score 1909; DB 11; Length 391;
Best Local Similarity 89.5%; Pred. No. 7.6e-169;
Matches 365; Conservative 10; Mismatches 15; Indels 18; Gaps 2;

QY 1 MAPSGRLRLPLLLPLWLVLTGPPAAGLSTCKTIDMELVKRRKRIEIRGOILSKRLA 60
Dd 1 MPPSGRLRLPLLLPLWLVLTGPPAAGLSTCKTIDMELVKRRKRIEIRGOILSKRLA 60
QY 61 SPPSGQGVPPGPLEPAVALYNSTRDRVAGESVEPEPEADYYAKEVTRVLMVESGNQI 120
Dd 61 SPPSGQGVPPGPLEPAVALYNSTRDRVAGESVEPEPEADYYAKEVTRVLMVETHHEI 120
QY 121 YDKFKGTGPHSLYMLFNTSELREAVPEPVLSSRAELRLRLKLVKEQHVELYQKYSNDSW 180
Dd 121 YDKFKQSTHSTYMFNISELREAVPEPVLSSRAELRLRLKLVKEQHVELYQKYSNNSW 180
QY 181 YLSNRLAPSDSPFWLSFDVTGVVROWLITRREATEGFRISAHSSSDSKDNTLHVEINGFN 240
Dd 181 YLSNRLAPSDSPFWLSFDVTGVVROWLITRREATEGFRISAHSCSDSDNTLQVDINGET 240
QY 241 SGRGDLATIHGMNRPFLILLMATPLERAQHLHSSRRRALDNTNSYPYDVPDYASLALDTN 300
Dd 241 TGRGDLATIHGMNRPFLILLMATPLERAQHLQSSRRR-----ALDTN 283
QY 301 YCFSSSTEKNCCVROLYIDFRKDLGKWKIHEPKGYHANFCLGPGCPYIWSLDTQYSKVLY 360
Dd 284 YCFSSSTEKNCCVROLYIDFRKDLGKWKIHEPKGYHANFCLGPGCPYIWSLDTQYSKVLY 343
QY 361 NOHNPASAAAPCCVPOALEPLPIVYVGRKPKVEQLSNMIVRSCKCS 407
Dd 344 NOHNPASAAAPCCVPOALEPLPIVYVGRKPKVEQLSNMIVRSCKCS 390

RESULT 9
US-09-214-592-28
; Sequence 28; Application US/09214592A
; Publication No. US20030027218A1
; GENERAL INFORMATION:
; APPLICANT: Yamasaki, Ckenj
; APPLICANT: Shibata, Ckenji
; APPLICANT: Sato, Ckenj
; TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND METHOD
; TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS
; FILE REFERENCE: 11060
; CURRENT APPLICATION NUMBER: US/09/214,592A
; CURRENT FILING DATE: 1999-01-18
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE:
; SEQ ID NO 28
; LENGTH: 390
; TYPE: PRT
; ORGANISM: canine
US-09-214-592-28

Query Match      87.7%; Score 1893.5; DB 11; Length 390;
Best Local Similarity 88.7%; Pred. No. 2.1e-167;
Matches 361; Conservative 12; Mismatches 17; Indels 17; Gaps 1;

QY 1 MAPSGRLRLPLLLPLWLVLTGPPAAGLSTCKTIDMELVKRRKRIEIRGOILSKRLA 60
Dd 1 MPPSGRLRLPLLLPLWLVLTGPPAAGLSTCKTIDMELVKRRKRIEIRGOILSKRLA 60
QY 61 SPPSGQGVPPGPLEPAVALYNSTRDRVAGESVEPEPEADYYAKEVTRVLMVESGNQI 120
Dd 61 SPPSGQGVPPGPLEPAVALYNSTRDRVAGESVEPEPEADYYAKEVTRVLMVENVNKI 120
QY 121 YDKFKGTGPHSLYMLFNTSELREAVPEPVLSSRAELRLRLKLVKEQHVELYQKYSNDSW 180
Dd 121 YEKVKKSPHSIYMLFNTSELREAVPEPVLSSRAELRLRLKLVKEQHVELYQKYSNDSW 180
QY 181 YLSNRLAPSDSPFWLSFDVTGVVROWLITRREATEGFRISAHSSSDSKDNTLHVEINGFN 240
Dd 181 YLSNRLAPSDIPEWLSFDVTGVVROWLITRREATEGFRISAHSCSDSDNTLQVDINGFS 240
QY 241 SGRGDLATIHGMNRPFLILLMATPLERAQHLHSSRRRALDNTNSYPYDVPDYASLALDTN 300
Dd 241 SSRGDLATIHGMNRPFLILLMATPLERAQHLHSSRRR-----ALDTN 283
QY 301 YCFSSSTEKNCCVROLYIDFRKDLGKWKIHEPKGYHANFCLGPGCPYIWSLDTQYSKVLY 360
Dd 284 YCFSSSTEKNCCVROLYIDFRKDLGKWKIHEPKGYHANFCLGPGCPYIWSLDTQYSKVLY 343
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[illegible]

QY 196 LSFDTGVVROWLTRREAEGLRLSAHSSSDSKDNTLHVEINGFSGRGDLATIHGMNR 255
DB 121 LSFDTGVVROWLTRREAEGLRLSAHSSSDSKDNTLQVINGFSGRGDLATIHGMNR 180
QY 256 PFLLMATPLERAQHLHSSRRALDTNYPYDVPDYASLALDTNYCFSSSTEKNCCVROL 315
DB 181 PFLLMATPLERAQHLHSSRR-----ALDTNYCFSSSTEKNCCVROL 223
QY 316 YIDFRKDLGKWNTHPKGYHAFNCPGLGCPYINSLDTQYSKVIALYNQHNPGASAPCCVP 375
DB 224 YIDFRKDLGKWNTHPKGYHAFNCPGLGCPYINSLDTQYSKVIALYNQHNPGASAPCCVP 283
QY 376 QALEPLPIVYVGRKPKVEQLSNMIVRSCKS 407
DB 284 QALEPLPIVYVGRKPKVEQLSNMIVRSCKS 315

RESULT 13
US-09-756-283A-20
; Sequence 20, Application US/09756283A
; Patent No. US20020151478A1
; GENERAL INFORMATION:
; APPLICANT: Chernajovsky, Yuti
; APPLICANT: Dreja, Hanna Stina
; APPLICANT: Adams, Gillian
; TITLE OF INVENTION: Latent Fusion Protein
; FILE REFERENCE: 0623.1000000
; CURRENT APPLICATION NUMBER: US/09/756,283A
; CURRENT FILING DATE: 2001-01-09
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LAP-mifn construct
US-09-756-283A-20

Query Match 58.5%; Score 1262.5; DB 10; Length 455;
Best Local Similarity 90.5%; Pred. No. 1.1e-108;
Matches 248; Conservative 10; Mismatches 15; Indels 1; Gaps 1;

QY 1 MAPSGLRLPLLLPLLWLVITGPPAAGLSTCKTIDMELVKRKRIEARGOILSKRLA 60
DB 1 MPESGLRLPLLLPLLWLVITGPPAAGLSTCKTIDMELVKRKRIEARGOILSKRLA 60
QY 61 SPSPGQDVPGLPEAVLALYNSTRVAGESVEPEPEADYAKVETRVLMVESGNOI 120
DB 61 SPSPGQDVPGLPEAVLALYNSTRVAGESVEPEPEADYAKVETRVLMVETHNEI 120
QY 121 YDKFKTGHSLYMLFNTSELREAVPEPVLLSRAELRL-RLKLVQHVHVELYOKYSNDSW 179
DB 121 YDKFKTGHSLYMLFNTSELREAVPEPVLLSRAELRLRLKLVQHVHVELYOKYSNDSW 180
QY 180 RYLSNRLAPSDPEWLSFDVTGVVQWLTTRRAIEGFRLSAHSSSDSKDNTLHVEINGF 239
DB 181 RYLSNRLAPSDPEWLSFDVTGVVQWLTTRRAIEGFRLSAHSSSDSKDNTLQVDINGF 240
QY 240 NSGRRGLATIHGMNRPFLMATPLERAQHLHS 273
DB 241 TTGRRGLATIHGMNRPFLMATPLERAQHLHS 274

RESULT 14
US-09-756-283A-22
; Sequence 22, Application US/09756283A
; Patent No. US20020151478A1
; GENERAL INFORMATION:
; APPLICANT: Chernajovsky, Yuti
; APPLICANT: Dreja, Hanna Stina
; APPLICANT: Adams, Gillian

; TITLE OF INVENTION: Latent Fusion Protein
; FILE REFERENCE: 0623.1000000
; CURRENT APPLICATION NUMBER: US/09/756,283A
; CURRENT FILING DATE: 2001-01-09
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mifn -LAP construct
US-09-756-283A-22

Query Match 52.8%; Score 1139; DB 10; Length 447;
Best Local Similarity 87.0%; Pred. No. 3.4e-97;
Matches 228; Conservative 10; Mismatches 18; Indels 6; Gaps 3;

QY 14 PL-LWLLVLTGPPAAGLSTCKTIDMELVKRKRIEARGOILSKRLASPPSQGDVPPGP 72
DB 190 PLGLW----AGGSAALSTCKTIDMELVKRKRIEARGOILSKRLASPPSQGEVPPGP 245
QY 73 LPEAVLALYNSTRVAGESVEPEPEADYAKVETRVLMVESGNOIYDKFKTGHSLY 132
DB 246 LPEAVLALYNSTRVAGESVEPEPEADYAKVETRVLMVETHNEIYDKFKQSTHSIY 305
QY 133 MLFNTSELREAVPEPVLLSRAELRL-RLKLVQHVHVELYOKYSNDSWRYLSNRLAPSD 191
DB 306 MFFNTSELREAVPEPVLLSRAELRLRLKLVQHVHVELYOKYSNNSWRYLSNRLAPSD 365
QY 192 SPEWLSFDVTGVVROWLTRRAIEGFRLSAHSSSDSKDNTLHVEINGFSGRGDLATIH 251
DB 366 SPEWLSFDVTGVVROWLTRRAIEGFRLSAHSSSDSKDNTLQVDINGFTTCRRGDLATIH 425
QY 252 GMRPFLMATPLERAQHLHS 273
DB 426 GMRPFLMATPLERAQHLHS 447

RESULT 15
US-09-214-592-32
; Sequence 32, Application US/09214592A
; Publication No. US20030027218A1
; GENERAL INFORMATION:
; APPLICANT: Yamasaki, Chotoo
; APPLICANT: Shibata, Kenji
; APPLICANT: Sato, Chisufumi
; TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND METHOD
; FILE REFERENCE: 11060
; CURRENT APPLICATION NUMBER: US/09/214,592A
; CURRENT FILING DATE: 1999-01-18
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE:
; SEQ ID NO 32
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Chicken
US-09-214-592-32

Query Match 48.5%; Score 1047; DB 11; Length 373;
Best Local Similarity 52.9%; Pred. No. 9.2e-89;
Matches 207; Conservative 52; Mismatches 100; Indels 32; Gaps 8;

QY 30 LSTCKTIDMELVKRKRIEARGOILSKRLASPPSQGDVPPCPPLPEAVLALYNSTRDVA 89
DB 2 LSTCKTIDMELVKRKRIEARGOILSKRLASPPSQGDVPPCPPLPEAVLALYNSTRDVA 61
QY 90 GFS-VEPEPEADYAKVETRVLMVESGNOIYDKFKTGHSLYMLFNTSELREAVPEPV 148
DB 62 QBARLRPPDGDDEYKAKELRIPMETTWGAMENHQPSHSIFVFNVSARRG-GHPT 120
QY 149 LLSRAELRLRLKLVQHVHVELYOKYSNDSWRYLSNRLAPSDSPEWLSFDVTGV 203

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OM protein - protein search, using sw model
Run on: October 7, 2003, 17:59:17 ; Search time 42 Seconds
(without alignments)
931.920 Million cell updates/sec

Title: US-10-017-372E-37
Perfect score: 2159
Sequence: 1 MAPSGRLPLLLPLLLLV.....GRKPKVEQLSNMIVRSKCS 407

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Maximum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2033.5	94.2	390	2 A27512	transforming growth
2	2002	92.7	391	2 S01413	transforming growth
3	1929.5	89.4	390	2 I46463	transforming growth
4	1916.5	88.8	390	1 WPHU2	transforming growth
5	1914.5	88.7	390	2 A26960	transforming growth
6	1893.5	87.7	390	2 JC4023	transforming growth
7	1835.5	85.0	390	1 WPM52	transforming growth
8	1835.5	85.0	390	2 S10219	transforming growth
9	1572.5	72.8	315	2 A40057	transforming growth
10	1047	48.5	373	2 A41918	transforming growth
11	871.5	40.4	412	2 A34939	transforming growth
12	868.5	40.2	382	2 B61036	transforming growth
13	834	38.6	409	2 S01825	transforming growth
14	827.5	38.3	410	2 A41397	transforming growth
15	826.5	38.3	410	2 A55706	transforming growth
16	824.5	38.2	412	2 A36189	transforming growth
17	824	38.2	414	1 WPM52	transforming growth
18	809	37.5	414	1 WPM52	transforming growth
19	809	37.5	414	2 A31249	transforming growth
20	808.5	37.4	413	1 WFXLB2	transforming growth
21	808	37.4	412	2 A39489	transforming growth
22	793	36.7	442	2 B31249	transforming growth
23	691.5	32.0	130	2 I48196	transforming growth
24	482	22.3	112	2 A61439	transforming growth
25	275	12.7	425	2 I47072	inhibin beta-A cha
26	272.5	12.6	424	1 WPM52	inhibin beta-A cha
27	270.5	12.5	424	1 S31440	inhibin beta-A cha
28	270	12.5	425	1 S50898	inhibin beta-A cha
29	268.5	12.4	426	1 B24248	inhibin beta-A cha

30	266.5	12.3	424	1 B40905	inhibin beta-A cha
31	256.5	11.9	513	1 BMHU6	bone morphogenetic
32	254.5	11.8	398	2 JH0688	bone morphogenetic
33	253.5	11.7	413	2 JC4862	activin beta-A cha
34	253	11.7	394	2 S45355	bone morphogenetic
35	253	11.7	398	2 JH0687	bone morphogenetic
36	252	11.7	396	1 BMHU2	bone morphogenetic
37	246	11.4	510	2 A54798	Vg-1-related prote
38	244.5	11.3	393	2 S37073	bone morphogenetic
39	243	11.3	455	2 A3918	TGF-beta-related p
40	238	11.0	350	2 JC5241	activin beta E cha
41	234.5	10.9	402	2 A45056	osteoegenic protein
42	231	10.7	420	2 I49541	bone morphogenetic
43	228	10.6	454	1 BMHU5	bone morphogenetic
44	227	10.5	367	2 JC4151	activin beta D cha
45	225.5	10.4	430	2 JQ1184	osteoegenic protein

ALIGNMENTS

RESULT 1
A27512
transforming growth factor beta-1 precursor - pig
N:Alternate names: TGF-beta
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 16-Jul-1999
C:Accession: A27512; A26356; I46657
R:Derynck, R.; Rhee, L.
Nucleic Acids Res. 15, 3187, 1987
A:Title: Sequence of the porcine transforming growth factor-beta precursor.
A:Reference number: A27512; MUID:87174844; PMID:3470708
A:Accession: A27512
A:Molecule type: mRNA
A:Residues: 1-390 <DER>
R:Chelifetz, S.; Weatherbee, J.A.; Tsang, M.L.S.; Anderson, J.K.; Mole, J.E.; Lucas, R.
Cell 48, 409-415, 1987
A:Title: The transforming growth factor-beta system, a complex pattern of cross-react
A:Reference number: A90890; MUID:87102890; PMID:2879635
A:Accession: A26356
A:Molecule type: protein
A:Residues: 279-322 <CHE>
R:Kondalah, P.; Van Oberghe-Schilling, E.; Ludwig, R.L.; Dhar, R.; Sporn, M.B.; Rob
J. Biol. Chem. 263, 18313-18317, 1988
A:Title: CDNA cloning of porcine transforming growth factor-beta 1 mRNAs. Evidence fo
A:Reference number: I46657; MUID:89054010; PMID:2461367
A:Accession: I46657
A>Status: preliminary: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-390 <KON>
A:Cross-references: GB:M23703; NID:g755044; PIDN:AAA64616.1; PID:g755045
C:Genetics:
A:Gene: TGFβ; TGF-beta-1
C:Superfamily: inhibin
C:Keywords: growth factor

Query Match		94.2%	Score 2033.5;	DB 2;	Length 390;
Best Local Similarity		95.1%	Pred. No. 6.9e-156;		
Matches 387;		Conservative	0;	Mismatches	3;
				Indels	17;
				Gaps	1;
Qy	1	MAPSGRLPLLLPLLLLVLTGPRPAAGLSTCKTIDMELVKRKRKEAIGQILSKRLA	60		
Db	1	MPPSGLRLLPLLLPLLLLVLTGPRPAAGLSTCKTIDMELVKRKRKEAIGQILSKRLA	60		
Qy	61	SPSQGDVPPGCLPEAVLALYNSTRDVACSEVPEPEPEADYAKETVRLVAVESNQI	120		
Db	61	SPRSQGDVPPGCLPEAVLALYNSTRDVACSEVPEPEPEADYAKETVRLVAVESNQI	120		
Qy	121	YDFKGTPTSHLYMIFNTSELREAVPEPVLLSRAELRLRLKLVQEHVELYQKYSNDSWR	180		
Db	121	YDFKGTPTSHLYMIFNTSELREAVPEPVLLSRAELRLRLKLVQEHVELYQKYSNDSWR	180		
Qy	181	YLSNRLAPSDSPSWLSFDVTGVVQWLTRREATIEGFRLSAHSSSDSKDNTLHVEINGFN	240		

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Db 181 YLSNRLAPSDSPWLSFDVTGVVQWLTREAEGLRLSAHSCSDKNTLHVEINGFN 240
Qy 241 SGRGDLATIHGMNRPFLLLMATPLERAQHLHSHRRRAALDNTSYDPDYASLADTN 300
Db 241 SGRGDLATIHGMNRPFLLLMATPLERAQHLHSHRRRAALDNTSYDPDYASLADTN 283
Qy 301 YCFSTSEKNCVROLYIDFRKDLGKWKIHEPKGYHANFCLGPGCPYIWSLDTQYSKVLAL 360
Db 284 YCFSTSEKNCVROLYIDFRKDLGKWKIHEPKGYHANFCLGPGCPYIWSLDTQYSKVLAL 343
Qy 361 QNHNPASAPCCVPQALEPPIVYVYGRKPKVQLSNMIVRSCKCS 407
Db 344 QNHNPASAPCCVPQALEPPIVYVYGRKPKVQLSNMIVRSCKCS 390

RESULT 2
S01413
transforming growth factor beta-1 precursor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 24-Nov-1999
C:Accession: S01413
R:Jakowlew, S.B.; Dillard, P.J.; Sporn, M.B.; Roberts, A.B.
Nucleic Acids Res. 16, 8730, 1988
A:Title: Nucleotide sequence of chicken transforming growth factor-beta 1 (TGF-beta 1).
A:Reference number: S01413; MUID:83335639; PMID:3166520
A:Accession: S01413
A:Molecule type: DNA
A:Residues: 1-391 <JAK>
A:Cross-references: EMBL:X12373; NID:963808; PIDN:CAA30933.1; PID:g63809
C:Superfamily: inhibin
C:Keywords: growth factor

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Query Match 92.7%; Score 2002; DB 2; Length 391;
Best Local Similarity 94.1%; Pred. No. 2.4e-153;
Matches 384; Conservative 0; Mismatches 6; Indels 18; Gaps 2;

Qy 1 MAPSGRLRLPLLLPLLLVLTGPRPAAGLSTCKTIDMELVKRKRIEIRGOILSKRLA 60
Db 1 MPPSGGLPLLLPLLLVLTGPRPAAGLSTCKTIDMELVKRKRIEIRGOILSKRLA 60
Qy 61 SPPSGQGVPPGPLEAVLALYNSTRDRVAGESVEPEPEADYAKEVTRVLMVESGNOI 120
Db 61 SPPSGQGVPPGPLEAVLALYNSTRDRVAGESVEPEPEADYAKEVTRVLMVESGNOI 120
Qy 121 YDKFKGTGPHSLYMLFNTSELREAVPEPVLISRAELRLRLKLVQEHVELYQKYSNDSWR 180
Db 121 YDKFKGTGPHSLYMLFNTSELREAVPEPVLISRAELRLRLKLVQEHVELYQKYSNDSWG 180
Qy 181 YLSNRLAPSDSPWLSFDVTGVVQWLTREAEGLRLSAHSSSDSKDNTLHVEIN-GF 239
Db 181 YLSNRLAPSDSPWLSFDVTGVVQWLTREAEGLRLSAHSCSDSKDNTLHVEINAGF 240
Qy 240 NSGRGDLATIHGMNRPFLLLMATPLERAQHLHSHRRRAALDNTSYDPDYASLADT 299
Db 241 NSGRGDLATIHGMNRPFLLLMATPLERAQHLHSHRRRAALDNTSYDPDYASLADT 283
Qy 300 NYCFSTSEKNCVROLYIDFRKDLGKWKIHEPKGYHANFCLGPGCPYIWSLDTQYSKVLAL 359
Db 284 NYCFSTSEKNCVROLYIDFRKDLGKWKIHEPKGYHANFCLGPGCPYIWSLDTQYSKVLAL 343
Qy 360 QNHNPASAPCCVPQALEPPIVYVYGRKPKVQLSNMIVRSCKCS 407
Db 344 QNHNPASAPCCVPQALEPPIVYVYGRKPKVQLSNMIVRSCKCS 391

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RESULT 3
I46463
transforming growth factor beta-1 - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 19-Dec-1997 #sequence_revision 19-Dec-1997 #text_change 24-Nov-1999
C:Accession: I46463; S45115
R:Woodall, C.J.; McLaren, L.J.; Watt, N.J.

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Gene 150, 371-373, 1994
A:Title: Sequence and chromosomal localisation of the gene encoding ovine latent tran
A:Reference number: I46463; MUID:95121932; PMID:7821809
A:Accession: I46463
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-390 <WOO>
A:Cross-references: EMBL:X76916; NID:g496648; PIDN:CAA54242.1; PID:g496649
A:Note: submitted to the EMBL Data Library, December 1993
C:Superfamily: inhibin

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Query Match 89.4%; Score 1929.5; DB 2; Length 390;
Best Local Similarity 89.7%; Pred. No. 1.6e-147;
Matches 365; Conservative 10; Mismatches 15; Indels 17; Gaps 1;

Qy 1 MAPSGRLRLPLLLPLLLVLTGPRPAAGLSTCKTIDMELVKRKRIEIRGOILSKRLA 60
Db 1 MPPSGRLRLPLLLPLLLVLTGPRPAAGLSTCKTIDMELVKRKRIEIRGOILSKRLA 60
Qy 61 SPPSGQGVPPGPLEAVLALYNSTRDRVAGESVEPEPEADYAKEVTRVLMVESGNOI 120
Db 61 SPPSGQGVPPGPLEAVLALYNSTRDRVAGESVEPEPEADYAKEVTRVLMVESGNOI 120
Qy 121 YDKFKGTGPHSLYMLFNTSELREAVPEPVLISRAELRLRLKLVQEHVELYQKYSNDSWR 180
Db 121 YDKFKGTGPHSLYMLFNTSELREAVPEPVLISRAELRLRLKLVQEHVELYQKYSNDSWR 180
Qy 181 YLSNRLAPSDSPWLSFDVTGVVQWLTREAEGLRLSAHSSSDSKDNTLHVEINGFN 240
Db 181 YLSNRLAPSDSPWLSFDVTGVVQWLTREAEGLRLSAHSCSDSKDNTLHVEINGFN 240
Qy 241 NSGRGDLATIHGMNRPFLLLMATPLERAQHLHSHRRRAALDNTSYDPDYASLADTN 300
Db 241 NSGRGDLATIHGMNRPFLLLMATPLERAQHLHSHRRRAALDNTSYDPDYASLADTN 283
Qy 301 NYCFSTSEKNCVROLYIDFRKDLGKWKIHEPKGYHANFCLGPGCPYIWSLDTQYSKVLAL 360
Db 284 NYCFSTSEKNCVROLYIDFRKDLGKWKIHEPKGYHANFCLGPGCPYIWSLDTQYSKVLAL 343
Qy 361 QNHNPASAPCCVPQALEPPIVYVYGRKPKVQLSNMIVRSCKCS 407
Db 344 QNHNPASAPCCVPQALEPPIVYVYGRKPKVQLSNMIVRSCKCS 390

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RESULT 4
WPHU2
transforming growth factor beta-1 precursor [validated]; - human
N:Alternate names: growth-inhibitory factor; TGF type 2; TGF-beta
C:Species: Homo sapiens (man)
C:Date: 28-Feb-1986 #sequence_revision 19-Oct-1995 #text_change 08-Dec-2000
C:Accession: A27513; A01395; A22290; I59664; S53444
R:Derynck, R.; Rhee, L.; Chen, E.Y.; Van Tilburg, A.
Nucleic Acids Res. 15, 3188-3189, 1987
A:Title: Intronic structure of the human transforming growth factor-beta precursor
A:Reference number: A27513; MUID:87174845; PMID:3470709
A:Accession: A27513
A:Molecule type: DNA
A:Residues: 1-390 <DER>
A:Cross-references: GB:X05839; GB:Y00112; NID:g37097; PIDN:CAA29283.1; PID:g1212989
R:Derynck, R.; Jarrett, J.A.; Chen, E.Y.; Eaton, D.H.; Bell, J.R.; Assoian, R.K.; Rob
Nature 316, 701-705, 1985
A:Title: Human transforming growth factor-beta complementary DNA sequence and express
A:Reference number: A01395; MUID:85296301; PMID:3861940
A:Accession: A01395
A:Molecule type: mRNA
A:Residues: 1-9,'p',11-24,'p',160-390 <DE2>
A:Cross-references: GB:X02812; GB:J05114; NID:g37092; PIDN:CAA26580.1; PID:g37093
A:Note: the authors suggest that residues 8-23 could represent the hydrophobic core o
R:Massague, J.; Like, B.
J. Biol. Chem. 260, 2636-2645, 1985
A:Title: Cellular receptors for type beta transforming growth factor. Ligand binding
A:Reference number: A22290; MUID:85131019; PMID:2982829
A:Accession: A22290

```

A:Molecule type: protein
A:Residues: 279-395 'XX', 298-301 <MAS>
R:Urushizaki, Y.; Nitsui, Y.; Teruti, T.; Koshida, Y.; Mahara, K.; Kohgo, Y.; Urushizaki, Tumor Res. 22, 41-55, 1987
A:Title: Cloning and expression of the gene for human transforming growth factor-beta in A:Reference number: I59664
A:Accession: I59664
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 279-390 <RES>
A:Cross-references: GB:M38449; NID:g339557; PIDN:AAA36735.1; PID:g339558
R:Stam, K.; Stewart, A.A.; Qu, G.Y.; Iwata, K.K.; Fenyo, D.; Chait, B.T.; Marshak, D.R. Blochem. J. 305, 87-92, 1995
A:Title: Physical and biological characterization of a growth-inhibitory activity purified A:Reference number: S53444; MUID:95126934; PMID:7826358
A:Accession: S53444
A:Status: preliminary
A:Molecule type: protein
A:Residues: 279-297 <STA>
C:Comment: The mature protein is the carboxyl-terminal segment of a precursor polypeptide C:Genetics:
A:Gene: GDB:TGFBI; TGFBI
A:Cross-references: GDB:120729; OMIM:190180
A:Map position: 19q13.2-19q13.2
C:Superfamily: inhibin
C:Keywords: glycoprotein; growth factor; homodimer; mitogen; transformation
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-278/Domain: propeptide #status predicted <PRO>
F:244-246/Region: cell attachment (R-G-D) motif
F:279-390/Product: cell attachment growth factor beta-1 #status experimental <MAT>
F:82.136.176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 88.8%; Score 1916.5; DB 1; Length 390;
Best Local Similarity 89.7%; Pred. No. 1.8e-146;
Matches 365; Conservative 10; Mismatches 15; Indels 17; Gaps 1;

Qy 1 MAPSGRLRLPLLLPLLLVLTPGRPAAGLSTCKTIDMELVKRKRIEIRGQILSKRLA 60
Db 1 MPSPGRLRLPLLLPLLLVLTPGRPAAGLSTCKTIDMELVKRKRIEIRGQILSKRLA 60
Qy 61 SPSPGQDVPPLPPLPAVALYNSTRDRVAGSEPEPEPEADYAKETRVLMVESGNOI 120
Db 61 SPSPGQEVPPGPIPEAVLALYNSTRDRVAGSEPEPEPEADYAKETRVLMVETHNEI 120
Qy 121 YDKFKGTPLSHLYMLNTSELREAVPEPVLLSRAELRLRLKLVQEHVELYQKYSNDSWR 180
Db 121 YDKFKQSTHSIYMFNTSELREAVPEPVLLSRAELRLRLKLVQEHVELYQKYSNNSWR 180
Qy 181 YLSNRLAPSDSPWLSFDVTGVVQWLTREAEGRFLSAHSSSDSKDNTLHVEINGFN 240
Db 181 YLSNRLAPSDSPWLSFDVTGVVQWLTREAEGRFLSAHSSSDSKDNTLQVDINGFT 240
Qy 241 SGRRGDLATIHGMNRPFLMATPLERAQHLHSSRRRALDNTSYDVPDYASLALDTN 300
Db 241 TGRRGDLATIHGMNRPFLMATPLERAQHLHSSRRRALDNTSYDVPDYASLALDTN 300
Qy 301 YCFSTENKCCVRQLYIDFRKDLGKWIHEPKGYHANFCLGCPPIVNSLDTQYSKVLY 360
Db 284 YCFSTENKCCVRQLYIDFRKDLGKWIHEPKGYHANFCLGCPPIVNSLDTQYSKVLY 343
Qy 361 NOHNPASAPCCVPQALPPIVYVGRKPKVEQLSNMIVRSCKS 407
Db 344 NOHNPASAPCCVPQALPPIVYVGRKPKVEQLSNMIVRSCKS 390

RESULT 6
JC4023
transforming growth factor beta-1 - dog
C:Species: Canis lupus familiaris (dog)
C:Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 24-Nov-1999
C:Accession: JC4023
R:Manning, A.M.; Auchampach, J.A.; Drong, R.F.; Slightom, J.L. Gene 155, 307-308, 1995
A:Title: Cloning of a canine cDNA homologous to the human transforming growth factor- A:Reference number: JC4023; MUID:95237630; PMID:772110
A:Accession: JC4023
A:Molecule type: mRNA
A:Residues: 1-390 <MAN>
A:Cross-references: GB:L34956; NID:g516071; PIDN:AAA51458.1; PID:g516072
C:Comment: This factor plays a multifunctional role as a regulator of mammalian cell C:Genetics:
A:Gene: tgf-beta1
C:Superfamily: inhibin
C:Keywords: growth factor; transforming protein
F:288-390/Product: transforming growth factor beta 1 #status predicted <MAT>

Query Match 87.7%; Score 1893.5; DB 2; Length 390;
Best Local Similarity 88.7%; Pred. No. 1.3e-144;
Matches 361; Conservative 12; Mismatches 17; Indels 17; Gaps 1;

Qy 1 MAPSGRLRLPLLLPLLLVLTPGRPAAGLSTCKTIDMELVKRKRIEIRGQILSKRLA 60
Db 1 MPSPGRLRLPLLLPLLLVLTPGRPAAGLSTCKTIDMELVKRKRIEIRGQILSKRLA 60

RESULT 5
A26960
transforming growth factor beta-1 precursor - green monkey
C:Species: Cercopithecus aethiops (green monkey, grivet)
C:Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 24-Nov-1999
C:Accession: A26960
R:Sharples, K.; Plowman, G.D.; Rose, T.M.; Twardzik, D.R.; Purchio, A.F. DNA 6, 239-244, 1987

A:Title: Cloning and sequence analysis of simian transforming growth factor-beta cDNA A:Reference number: A26960; MUID:67246074; PMID:3474130
A:Accession: A26960
A:Molecule type: mRNA
A:Residues: 1-390 <SHA>
A:Cross-references: GB:M16658; NID:g176552; PIDN:AAA35369.1; PID:g176553
C:Superfamily: inhibin
C:Keywords: growth factor
F:1-16/Domain: signal sequence #status predicted <SIG>
F:17-390/Product: transforming growth factor beta #status predicted <MAT>

Query Match 88.7%; Score 1914.5; DB 2; Length 390;
Best Local Similarity 89.4%; Pred. No. 2.6e-146;
Matches 364; Conservative 10; Mismatches 16; Indels 17; Gaps 1;

Qy 1 MAPSGRLRLPLLLPLLLVLTPGRPAAGLSTCKTIDMELVKRKRIEIRGQILSKRLA 60
Db 1 MPSPGRLRLPLLLPLLLVLTPSRPAAGLSTCKTIDMELVKRKRIEIRGQILSKRLA 60
Qy 61 SPSPGQDVPPLPPEAVLALYNSTRDRVAGSEPEPEPEADYAKETRVLMVESGNOI 120
Db 61 SPSPGQEVPPGPIPEAVLALYNSTRDRVAGSEPEPEPEADYAKETRVLMVETHNEI 120
Qy 121 YDKFKGTPLSHLYMLNTSELREAVPEPVLLSRAELRLRLKLVQEHVELYQKYSNDSWR 180
Db 121 YDKFKQSTHSIYMFNTSELREAVPEPVLLSRAELRLRLKLVQEHVELYQKYSNNSWR 180
Qy 181 YLSNRLAPSDSPWLSFDVTGVVQWLTREAEGRFLSAHSSSDSKDNTLHVEINGFN 240
Db 181 YLSNRLAPSDSPWLSFDVTGVVQWLTREAEGRFLSAHSSSDSKDNTLQVDINGFT 240
Qy 241 SGRRGDLATIHGMNRPFLMATPLERAQHLHSSRRRALDNTSYDVPDYASLALDTN 300
Db 241 TGRRGDLATIHGMNRPFLMATPLERAQHLHSSRRRALDNTSYDVPDYASLALDTN 300
Qy 301 YCFSTENKCCVRQLYIDFRKDLGKWIHEPKGYHANFCLGCPPIVNSLDTQYSKVLY 360
Db 284 YCFSTENKCCVRQLYIDFRKDLGKWIHEPKGYHANFCLGCPPIVNSLDTQYSKVLY 343
Qy 361 NOHNPASAPCCVPQALPPIVYVGRKPKVEQLSNMIVRSCKS 407
Db 344 NOHNPASAPCCVPQALPPIVYVGRKPKVEQLSNMIVRSCKS 390

Db 283 IDFRKDLQMKWIHEPKGYMAIFCMGCPYIWSADTQYIKVLYLNQHNPGASAAAPCCVPQ 342

QY 377 ALPPLPIVYVGRKPKVEQLSNMIVRSCKCS 407

Db 343 TLDPLPIIYVYVGRNVRVEQLSNMIVRSCKCS 373

RESULT 11

A34939

Transforming growth factor beta-3 precursor - chicken

C:Species: Gallus gallus (chicken)

C:Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 16-Jul-1999

C:Accession: A34939; S36125; S36124; I51181

R:Jakowlew, S.B.; Dillard, P.J.; Kondaiah, P.; Sporn, M.B.; Roberts, A.B.

Mol. Endocrinol. 2, 747-755, 1988

A:Title: Complementary deoxyribonucleic acid cloning of a novel transforming growth factor

A:Reference number: A34939; MUID:89096966; PMID:3211158

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-412 <JAK>

A:Cross-references: GB:M31154; NID:g212758; PIDN:AAA49089.1; PID:g212759

R:Burt, D.W.; Paton, I.R.; Dey, B.X.

J. Mol. Endocrinol. 7, 175-183, 1991

A:Title: Comparative analysis of human and chicken transforming growth factor-beta-2 and

A:Reference number: S25850; MUID:93134496; PMID:1840616

A:Accession: S25850

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 119-172 <BU2>

A:Cross-references: EMBL:X60055; NID:g396688; PIDN:CAA42653.1; PID:g396689

A:Note: The nucleotide sequence was submitted to the EMBL Data Library, June 1991

A:Accession: S36124

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 173-322, 'ELPT', 327-412 <BU3>

A:Cross-references: EMBL:X60091

A:Note: The nucleotide sequence was submitted to the EMBL Data Library, June 1991

R:Jakowlew, S.B.; Lechleider, R.; Geisler, A.G.; Kim, S.J.; Santa-Coloma, T.A.; Cubert, J.

Mol. Endocrinol. 6, 1285-1298, 1992

A:Title: Identification and characterization of the chicken transforming growth factor-h

A:Reference number: I51181; MUID:93024487; PMID:1406706

A:Accession: I51181

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-117 <JA2>

A:Cross-references: GB:S46000; NID:g257172; PIDN:AAB23575.1; PID:g257173

C:Genetics:

A:Introns: 216/1; 252/1; 309/2; 363/3

A:Note: list of introns may be incomplete

C:Superfamily: inhibin

C:Keywords: glycoprotein; growth factor; growth regulation; homodimer; mitogen

F:1-22/Domain: signal sequence #status predicted <SIG>

F:23-300/Domain: propeptide #status predicted <PRO>

F:301-412/product: transforming growth factor beta-3 #status predicted <MAT>

F:74,142/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 40.4%; Score 871.5; DB 2; Length 412;

Best Local Similarity 46.2%; Pred. No. 2.6e-62;

Matches 198; Conservative 56; Mismatches 114; Indels 61; Gaps 14;

QY 15 LVLVLVTPGPAAGLSTCKTIDMELVKRRIEAIHQILSKLASPPSGVPPGGLP 74

Db 9 LVLSLSLFAVLSLASCITLDLHLKXKVRVIAHQILSKLRLTSPPE--SVGPAHP 66

QY 75 BAVIALYNSTRDRVAGSEVEPE-----PEADYAKVEYTRVLMVE--SGNQIYDKF 124

Db 67 YQILALYNSTRLL--BEMEBEKESQNTSEYAKETHKFDMDIQTGLPEHNLGICP 124

QY 125 KGTPHSLYMLENTSELREAVPEPVLLSRAELRLRL---KLKVEOHVELYQKYSND--- 177

Db 125 KGVTSNVFR-FNVS---SAEKNSTNLFRAEFLVRLVNPSPSSKRSEORIELFOILRPDEHI 180

QY 178 -SWRYLSNRLAPSDSPWLSFDVTGVVQWQTRREAIEGFRLSAH-----SSSDSKD 229

Db 181 AKORYLSGRNVOTRGSPWLSFDVTGVRELLHRESNLGLAISIHCPCHTQPNQDILE 240

QY 230 N---TLHVEINGFNSG---RRGLATI---HGMNRPFLMATPLERAOH--LHSSRRH 278

Db 241 NLHVELEIKFGIDSEDDYGRDGLRKLKQKDLNPHLILMMLPPHRLSEPTLGGQRKR 300

QY 279 ALDTSNYPYDVPDYASALADTNYCFSTSEKNCPCPOLYIDFRKDLGKWKWIHEPKGYHANF 338

Db 301 -----ALDNYCFNLEENCVRPLYIDFRQDLGKWKVHEPKGYFANF 343

QY 339 CLGCPYIWSLDTQYKSVLYLNQHNPGASAAAPCCVPQALEPLPIVYVYVGRKPKVEQLSN 398

Db 344 CSQPCPYLSADTTHSTVLGLYNILNPEASAPCCVPQDLEPLTILYVYVGRTPKVEQLSN 403

QY 399 MIVRSCKCS 407

Db 404 MYVRSCKCS 412

RESULT 12

B61036

Transforming growth factor beta-5 precursor - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C:Date: 31-Dec-1993 #sequence_revision 03-Feb-1994 #text_change 16-Jul-1999

C:Accession: A34929; B61036

R:Kondaiah, P.; Sands, M.J.; Smith, J.M.; Fields, A.; Roberts, A.B.; Sporn, M.B.; Mel

J. Biol. Chem. 265, 1089-1093, 1990

A:Title: Identification of a novel transforming growth factor-beta (TGF-beta5) mRNA i

A:Reference number: A34929; MUID:90110090; PMID:2295601

A:Accession: A34929

A:Molecule type: mRNA

A:Residues: 1-382 <KON>

A:Cross-references: GB:J05180; NID:g214821; PIDN:AAA49968.1; PID:g214822

R:Roberts, A.B.; Rosa, F.; Roche, N.S.; Coligan, J.E.; Garfield, M.; Rebbert, M.L.; K

Growth Factors 2, 135-147, 1990

A:Title: Isolation and characterization of TGF-beta2 and TGF-beta5 from medium condit

A:Reference number: A61036; MUID:90253806; PMID:2340184

A:Accession: B61036

A:Molecule type: protein

A:Residues: 271-276, 'X', 278-284, 'XX', 287-299 <ROB>

C:Superfamily: inhibin

C:Keywords: growth factor

F:271-382/Product: transforming growth factor beta-5 #status experimental <MAT>

Query Match 40.2%; Score 868.5; DB 2; Length 382;

Best Local Similarity 45.9%; Pred. No. 4e-62;

Matches 190; Conservative 55; Mismatches 122; Indels 47; Gaps 11;

QY 9 LPLLPLMLLVLTGCPGPAAGLSTCKTIDMELVKRRIEAIHQILSKLASPPSGQGV 68

Db 1 MEVLMMLLVLLVHLSSLSLSTCRVDMEEYKRRRIEAIHQILSKLKDTPDV-DS 59

QY 69 PPGLPEAVLYLNSTRDRVAGSEVEPE-----PEPEADYAKVEYTRVLMVESGNIYDK 123

Db 60 EKMTPVSEAFILYNSTLEIVIREKATREEHVGHQNDIQYAKQVYR---FESITLED- 115

QY 124 FKGTPHSLYMLENTSELREAVPEPVLLSRAELRLRLKL--KYEQHVELYQKYSNDSW-- 179

Db 116 -----HEFKFKFNASHVRENVMNSLHLHAELRMYKQTDKNKDQRMELFQYQENGTH 170

QY 180 -RYLSNRLAPSDSPWLSFDVTGVVQWQTRREAIEGFRLSAH-----SSSDSKDNLHVE 235

Db 171 SRYLESKYITPVTDDEWMSFDVTGVVQWQTRREAIEGFRLSAH-----SSSDSKDNLHVE 226

QY 236 INGNFSRRGRGLATIHGM---NRPFLLMATPLERAOHLHSSRRHRLDNTNSYDVPDYA 293

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OM protein - protein search, using sw model

Run on: October 7, 2003, 17:52:07 ; Search time 23 seconds
(without alignments)
832.168 Million cell updates/sec

Title: US-10-017-372E-37

Perfect score: 2159
Sequence: 1 MAPSGRLRLPLLLPLLLLV.....GRKPKVEQLNMIVRSCKCS 407

Scoring table: BLOSUM62
Gapop 10.0 , Capext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2030.5	94.0	390	1	TGFL_PIG
2	1929.5	89.4	390	1	TGFL_PIG
3	1916.5	88.8	390	1	TGFL_PIG
4	1914.5	88.7	390	1	TGFL_PIG
5	1893.5	87.7	390	1	TGFL_PIG
6	1899.5	85.2	390	1	TGFL_PIG
7	1835.5	85.0	390	1	TGFL_PIG
8	1835.5	85.0	390	1	TGFL_PIG
9	1826.5	84.6	390	1	TGFL_PIG
10	1572.5	72.8	315	1	TGFL_PIG
11	1047	48.5	373	1	TGFL_PIG
12	868.5	40.2	382	1	TGFL_PIG
13	852.5	39.5	412	1	TGFL_PIG
14	834	38.6	409	1	TGFL_PIG
15	827.5	38.3	410	1	TGFL_PIG
16	826.5	38.3	412	1	TGFL_PIG
17	824.5	38.2	412	1	TGFL_PIG
18	824	38.2	414	1	TGFL_PIG
19	809	37.5	414	1	TGFL_PIG
20	808.5	37.4	413	1	TGFL_PIG
21	808	37.4	412	1	TGFL_PIG
22	805	37.3	435	1	TGFL_PIG
23	805	37.3	442	1	TGFL_PIG
24	482	22.3	412	1	TGFL_PIG
25	323.5	15.0	375	1	TGFL_PIG
26	321.5	14.9	375	1	TGFL_PIG
27	311.5	14.4	375	1	TGFL_PIG
28	310.5	14.4	375	1	TGFL_PIG
29	308.5	14.3	376	1	TGFL_PIG
30	307.5	14.2	375	1	TGFL_PIG
31	306.5	14.2	376	1	TGFL_PIG
32	305.5	14.2	375	1	TGFL_PIG
33	300	13.9	405	1	TGFL_PIG

34	300	13.9	407	1	GDFB_HUMAN
35	296.5	13.7	375	1	GDFB_BOVIN
36	280.5	13.0	374	1	GDFB_BRARE
37	278.5	12.9	345	1	GDFB_RAT
38	275	12.7	425	1	IHBA_SHEEP
39	272.5	12.6	424	1	IHBA_PIG
40	270.5	12.5	424	1	IHBA_MOUSE
41	270.5	12.5	424	1	IHBA_RAT
42	270	12.5	425	1	IHBA_BOVIN
43	269.5	12.5	426	1	IHBA_HORSE
44	268.5	12.4	426	1	IHBA_HUMAN
45	265.5	12.3	424	1	IHBA_CHICK

ALIGNMENTS

RESULT 1	
TGFL_PIG	
ID	TGFL_PIG
AC	P07200; P08832; STANDARD; PRT; 390 AA.
DT	01-APR-1988 (Rel. 07, Created)
DT	01-APR-1988 (Rel. 07, Last sequence update)
DT	28-FEB-2003 (Rel. 41, Last annotation update)
DE	Transforming growth factor beta 1 precursor (TGF-beta 1).
GN	TGFB1.
OS	Sus scrofa (Pig).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX	NCBI_TaxID=9823;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Ovary;
RX	MEDLINE=87174844; PubMed=3470708;
RA	Derynck R., Rhee L.;
RT	"Sequence of the porcine transforming growth factor-beta precursor.";
RL	Nucleic Acids Res. 15:3187-3187(1987).
RN	[2]
RP	SEQUENCE FROM N.A., AND VARIANT VAL-114.
RC	STRAIN-Miniature swine;
RX	MEDLINE=89054010; PubMed=2461367;
RA	Kondalah P., van Obberghen-Schilling E., Ludwig R.L., Dhar R.,
RT	Sporn M.B., Roberts A.B.;
RT	"cDNA cloning of porcine transforming growth factor-beta 1 mRNAs.
RT	Evidence for alternate splicing and polyadenylation.";
RL	J. Biol. Chem. 263:18313-18317(1988).
RN	[3]
RP	SEQUENCE FROM N.A., AND VARIANT VAL-114.
RX	MEDLINE=88335639; PubMed=3166520;
RA	Jakowlew S.B., Dillard P.J., Sporn M.B., Roberts A.B.;
RT	"Nucleotide sequence of chicken transforming growth factor-beta 1
RT	(TGF-beta 1).";
RL	Nucleic Acids Res. 16:8730-8730(1988).
RN	[4]
RP	SHOWS THAT REF.3 SEQUENCE IS FROM PIG.
RA	Jakowlew S.B.;
RT	Unpublished observations (MAR-1996).
RN	[5]
RP	SEQUENCE FROM N.A., AND VARIANT VAL-114.
RA	Wimmers K., Chomdej S., Ponsuksili S., Schellander K.;
RT	"Polymorphism in the porcine transforming growth factor beta 1
RT	gene.";
RL	Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN	[6]
RP	SEQUENCE OF 279-322.
RX	MEDLINE=87102890; PubMed=2879635;
RA	Cheifetz S., Weatherbee J.A., Tsang M.L.S., Anderson J.K., Mole J.E.,
RT	Lucas R., Massague J.;
RT	"The transforming growth factor-beta system, a complex pattern of
RT	cross-reactive ligands and receptors.";
RL	Cell 48:409-415(1987).
CC	-1- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
CC	PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL

```
CC CC TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
CC CC HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
CC CC ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
CC CC A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC CC
CC CC -1- SUBUNIT: Homodimer; disulfide-linked.
CC CC -1- SIMILARITY: Belongs to the TGF-beta family.
CC CC -1- CAUTION: REF.3 SEQUENCE WHICH WAS SAID TO ORIGINATE FROM CHICKEN
CC CC WHITE LEGHORN, SEEMS (REF.4) TO ORIGINATE FROM PIG.
CC CC
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CC CC or send an email to license@isb-sib.ch).
CC CC -----
CC CC EMBL; Y00111; CAA68291.1; -.
CC CC EMBL; M23703; AAA64616.1; -.
CC CC EMBL; X12373; CAA30933.1; -.
CC CC EMBL; AF461808; AAL57902.1; -.
CC CC PIR; A27512; A27512.
CC CC HSSP; P01137; IKLA.
CC CC InterPro; IPR002400; GF_cysknot.
CC CC InterPro; IPR003911; TGF_TGFB.
CC CC InterPro; IPR001839; TGFB.
CC CC InterPro; IPR001111; TGFB.N.
CC CC Pfam; PF00019; TGF-beta: 1.
CC CC Pfam; PF00688; TGFb_propeptide: 1.
CC CC PRINTS; PR00438; GFCYSKNOT.
CC CC PRINTS; PR01423; TGFbeta.
CC CC ProDom; PD000357; TGFB; 1.
CC CC SMART; SM00204; TGFB; 1.
CC CC PROSITE; PS00250; TGF_BETA_1; 1.
CC CC Growth factor; Mitogen; Glycoprotein; Signal; Polymorphism.
CC CC SIGNAL
CC CC 1 23
CC CC 24 278
CC CC FT CHAIN 279 390 TRANSFORMING GROWTH FACTOR BETA 1.
CC CC FT DISULFID 285 294 BY SIMILARITY.
CC CC FT DISULFID 293 356 BY SIMILARITY.
CC CC FT DISULFID 322 387 BY SIMILARITY.
CC CC FT DISULFID 326 389 BY SIMILARITY.
CC CC FT DISULFID 355 355 INTERCHAIN (BY SIMILARITY).
CC CC FT CARBOHYD 82 82 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CC FT CARBOHYD 136 136 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CC FT CARBOHYD 176 176 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CC FT SITE 244 246 CELL ATTACHMENT SITE (POTENTIAL).
CC CC FT VARIANT 114 114 L -> V.
CC CC FT CONFLICT 6 7 LR -> PG (IN REF. 3).
CC CC FT CONFLICT 180 180 R -> G (IN REF. 3).
CC CC FT CONFLICT 237 237 N -> NA (IN REF. 3).
CC CC SEQUENCE 390 AA; 44294 MW; A6E2C3659FC384E6 CRC64;
CC CC
CC CC Query Match 94.0%; Score 2030.5; DB 1; Length 390;
CC CC Best Local Similarity 94.8%; Pred. No. 7.3e-153;
CC CC Matches 386; Conservative 1; Mismatches 3; Indels 17; Gaps 1;
CC CC
CC CC QY 1 MAPSGRLRLPLLLPLLLVLTGPPAAGLSTCKTIDMELVKRRKRIEAIQGILSKRLA 60
CC CC 1 MPSPGRLRLPLLLPLLLVLTGPPAAGLSTCKTIDMELVKRRKRIEAIQGILSKRLA 60
CC CC
CC CC 61 SPSPGSDVPPGGLPAVALVLTNSTRDVRAGESVEPEPEADYAKETRVLMVSGNQI 120
CC CC 61 SPSPGSDVPPGGLPAVALVLTNSTRDVRAGESVEPEPEADYAKETRVLMVSGNQI 120
CC CC
CC CC 121 YDKFKGTPHSLMYLNTSELREAVPEPVLLSRAELRLRLKLVQHVLYQKYSNDSWR 180
CC CC 121 YDKFKGTPHSLMYLNTSELREAVPEPVLLSRAELRLRLKLVQHVLYQKYSNDSWR 180
CC CC
CC CC 181 YLSNRLAPSDSPENLSFDYTGVRQWLTTRRAIEGFRLSAHSSDSDKNTLHVEINGFN 240
CC CC 181 YLSNRLAPSDSPENLSFDYTGVRQWLTTRRAIEGFRLSAHSSDSDKNTLHVEINGFN 240
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QY 241 SRRGDLATHGMNRPFLLLMATPLERAQHLHSSRRRALDTNSPYDVPDYASLALDTN 300
DB 241 SRRGDLATHGMNRPFLLLMATPLERAQHLHSSRRRALDTNSPYDVPDYASLALDTN 283
QY 301 YCFSTSEKNCVROLYIDFRKDLGKWIHEPKGYHANFCLGCPQYIWSLDTQYSKVLALY 360
DB 284 YCFSTSEKNCVROLYIDFRKDLGKWIHEPKGYHANFCLGCPQYIWSLDTQYSKVLALY 343
QY 361 NQHPGASAPCCVPOALEPLPIYVYVGRPKVQEQLSNMIVRSCKCS 407
DB 344 NQHPGASAPCCVPOALEPLPIYVYVGRPKVQEQLSNMIVRSCKCS 390

RESULT 2
TGFL_SHEEP STANDARD; PRT: 390 AA.
AC P50414;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Transforming growth factor beta 1 precursor (IGF-beta 1).
GN TGFB1.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
CX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95121932; PubMed=7821809;
RA Woodall C.J., McIaren I.J., Watt N.J.;
RT "Sequence and chromosomal localisation of the gene encoding ovine
RL Gene 150:371-373(1994).
RN [2]
RP SEQUENCE OF 281-390 FROM N.A.
RC STRAIN=Merino; TISSUE=Skin;
RX MEDLINE=95268698; PubMed=7749621;
RA Sutton R., Ward W.G., Raphael K.A., Cam G.R.;
RT "Growth factor expression in skin during wool follicle development.";
RL Comp. Biochem. Physiol. 110B:697-705(1995).
CC -1- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
CC PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
CC HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
CC ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
CC A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC -1- SUBUNIT: Homodimer; disulfide-linked.
CC -1- SIMILARITY: Belongs to the TGF-beta family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X76916; CAA54242.1; -.
CC EMBL; L36038; AAA31526.1; -.
CC PIR; I46453; I46463.
CC HSSP; P01137; IKLA.
CC InterPro; IPR002400; GF_cysknot.
CC InterPro; IPR003911; TGF_TGFB.
CC InterPro; IPR001839; TGFB.
CC InterPro; IPR001111; TGFB.N.
CC Pfam; PF00019; TGF-beta: 1.
CC Pfam; PF00688; TGFb_propeptide: 1.
CC PRINTS; PR00438; GFCYSKNOT.
CC PRINTS; PR01423; TGFbeta.
CC ProDom; PD000357; TGFB; 1.
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DR SMART: SM00204; TGFβ: 1.
DR PROSITE: PS00250; TGFβ_BETA_1; 1.
RW Growth factor; Mitogen; Glycoprotein; Signal.
FT SIGNAL 1 23
FT PROPEP 24 278
FT CHAIN 279 390
FT DISULFID 285 294
FT DISULFID 293 356
FT DISULFID 322 387
FT DISULFID 326 389
FT DISULFID 355 355
FT CARBOHYD 82 82
FT CARBOHYD 136 136
FT CARBOHYD 176 176
FT SITE 244 246
SQ SEQUENCE 390 AA; 44291 MW; 1C247299484D0E57 CRC64;

Query Match 89.4%; Score 1929.5; DB 1; Length 390;
Best Local Similarity 89.7%; Pred. No. 6.8e-145;
Matches 365; Conservative 10; Mismatches 15; Indels 17; Gaps 1;

QY 1 MAPSGRLRLPLLLPLMLLVLTPGPAAGLSTCKTIDMELVKRRRIEAIHQILSKRLA 60
DB 1 MPSPGLRLPLLLPLMLLVLTPGPAAGLSTCKTIDMELVKRRRIEAIHQILSKRLA 60
QY 61 SPSPGQDVPGLPEAVLALYNSTRDVRAGSEPEPEADYAKETRVLMVYEGNQI 120
DB 61 SPSPGQDVPGLPEAVLALYNSTRDVRAGSEPEPEADYAKETRVLMVYEGNQI 120
QY 121 YDKFKGTGPHSLYMLFNTSELREAVPEPVLSSRAELRLRLKLVQHVLYQKYSNDSWR 180
DB 121 YDKMKSSHSYMFNTSELREAVPEPVLSSRAELRLRLKLVQHVLYQKYSNDSWR 180
QY 181 YLSNRLAPSDPEWLSFVYGVVQWLTREAIIEGFLSAHSSDSKNTLHVEINGFN 240
DB 181 YLSNRLAPSDPEWLSFVYGVVQWLTREAIIEGFLSAHSSDSKNTLHVEINGFN 240
QY 241 SGRRGLATIGHMNPFLLLMATPLERAGHLSSRRRLALDNTSYPDVQVYASIALDTN 300
DB 241 SGRRGLATIGHMNPFLLLMATPLERAGHLSSRRRLALDNTSYPDVQVYASIALDTN 300
QY 301 YCFSTEKNCCVQQLYIDFRKDLGKWKIHEPKGYHANFCLGCPPIWISLDTOYSKVLALY 360
DB 284 YCFSTEKNCCVQQLYIDFRKDLGKWKIHEPKGYHANFCLGCPPIWISLDTOYSKVLALY 343
QY 361 NOHNPQASAPCCVQQALESPLIVYVGVKPKVQGLSNMIVRSCKS 407
DB 344 NOHNPQASAPCCVQQALESPLIVYVGVKPKVQGLSNMIVRSCKS 390

RESULT 3
TGFβ_HUMAN
ID TGFβ_HUMAN STANDARD; PRT; 390 AA.
AC P01137; Q9UGG4;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Transforming growth factor beta 1 precursor (TGF-beta 1).
GN TGFβ1 OR TGFβ.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87174845; PubMed=3470709;
RA Derynck R., Rhee L., Chen E.Y., van Tilburg A.;
RA "Intron-exon structure of the human transforming growth factor-beta
precursor gene.";
RL Nucleic Acids Res. 15:3188-3189(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=85296301; PubMed=3861940;
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RA Derynck R., Jarrett J.A., Chen E.Y., Eaton D.H., Bell J.R.,
RA Assoian R.K., Roberts A.B., Sporn M.B., Goeddel D.V.;
RT "Human transforming growth factor-beta complementary DNA sequence and
expression in normal and transformed cells.";
RL Nature 316:701-705(1985).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Ductum, and Eye;
MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse J.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner I., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusica K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF 279-390 FROM N.A.
RX TISSUE=Carcinoma;
RA Urushizaki Y., Niitsu Y., Terui T., Koshida Y., Mahara K., Kohgo Y.,
RT "Cloning and expression of the gene for human transforming growth
factor-beta in Escherichia coli.";
RL Tumor Res. 22:41-55(1987).
RN [5]
RP SEQUENCE OF 279-329.
RX TISSUE=Bladder carcinoma;
RA Bourdrel L., Lin C.-H., Lauren S.L., Elmore R.H., Sugarman B.J.,
RA Hu S., Westcott K.R.;
RT "Recombinant human transforming growth factor-beta 1: expression by
Chinese hamster ovary cells, isolation, and characterization.";
RL protein Expr. Purif. 4:130-140(1993).
RN [6]
RP SEQUENCE OF 279-301.
RX MEDLINE=85131019; PubMed=2982829;
RA Massague J., Like B.;
RT "Cellular receptors for type beta transforming growth factor. Ligand
binding and affinity labeling in human and rodent cell lines.";
RL J. Biol. Chem. 260:2636-2645(1985).
RN [7]
RP STRUCTURE BY NMR OF 279-390.
RX MEDLINE=93144319; PubMed=842942;
RA Archer S.J., Bax A., Roberts A.B., Sporn M.B., Ogawa Y., Piez K.A.,
RA Weatherbee J.A., Tsang M.L.-S., Lucas R., Zheng B.-L., Wenker J.,
RA Torchia D.A.;
RT "Transforming growth factor beta 1: NMR signal assignments of the
recombinant protein expressed and isotopically enriched using Chinese
hamster ovary cells.";
RL Biochemistry 32:1152-1163(1993).
RN [8]
RP STRUCTURE BY NMR OF 279-390.
RX MEDLINE=93144320; PubMed=842943;
RA Archer S.J., Bax A., Roberts A.B., Sporn M.B., Ogawa Y., Piez K.A.,
RA Weatherbee J.A., Tsang M.L.-S., Lucas R., Zheng B.-L., Wenker J.,
RA Torchia D.A.;
RT "Transforming growth factor beta 1: secondary structure as determined
by heteronuclear magnetic resonance spectroscopy.";
RL Biochemistry 32:1164-1171(1993).
RN [9]
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CC -!- SUBUNIT: Homodimer; disulfide-linked.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the TGF-beta family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M16658; AAA35369.1; -.
CC PR: A26960; A26960.
CC HSP: P01137; IKLA.
CC InterPro: IPR002400; GF_cysknot.
CC InterPro: IPR003911; TGF_TGFB.
CC InterPro: IPR001839; TGFB.
CC InterPro: IPR001111; TGFB_N.
CC Pfam: PF00019; TGF-beta; 1.
CC Pfam: PF00688; TGFB_propeptide; 1.
CC PRINTS: PR00438; GFCYSKNOT.
CC ProDom: PD000357; TGFB; 1.
CC SMART: SM00204; TGFB; 1.
CC PROSITE: PS00250; TGF_BETA_1; 1.
CC Growth factor; Mitogen; Glycoprotein; Signal.
CC SIGNAL 16 POTENTIAL.
CC FT PROPEP 17 278
CC FT CHAIN 279 390
CC FT DISULFID 285 294
CC FT DISULFID 293 356
CC FT DISULFID 322 387
CC FT DISULFID 326 389
CC FT DISULFID 355 355
CC FT CARBOHYD 82 82
CC FT CARBOHYD 136 136
CC FT CARBOHYD 176 176
CC FT SITE 244 246
CC SEQUENCE 390 AA; 44356 MW; DPF63E2BAB44320E CRC64;

Query Match 88.7%; Score 1914.5; DB 1; Length 390;
Best Local Similarity 89.4%; Pred. No. 1e-143;
Matches 364; Conservative 10; Mismatches 16; Indels 17; Gaps 1;

Oy 1 MAPSGRLRLPLLLPLLLVLTGCPAAGLSTCKTIDMEVAKRRIEAIKQILSKRLA 60
Db 1 MPSPGLRLPLLLPLLLVLTGCPAAGLSTCKTIDMEVAKRRIEAIKQILSKRLA 60
Oy 61 SPSPGQGVPPGPLPAVLALYNSTRDRVAGSEPEPEPEADYAKVTRVLWVESGHOI 120
Db 61 SPSPGQGVPPGPLPAVLALYNSTRDRVAGSEPEPEPEADYAKVTRVLWVTHNEI 120
Oy 121 YDKFKGTPHSYMLFNTSELREAVPEPVLLSRAELRLRLKLKVEQHVLYKYSNDSWR 180
Db 121 YDKFKGTSTHYMFNTSELREAVPEPVLLSRAELRLRLKLKVEQHVLYKYSNDSWR 180
Oy 181 YLSNRLAPSPEWLSFDVGVVQWLTREATEGFRLSAHSSDSKNTLHVEINGFN 240
Db 181 YLSNRLAPSPEWLSFDVGVVQWLTREATEGFRLSAHSSDSKNTLQVDINGFT 240
Oy 241 SGRRGDLATIGHMNPFLLLMATPLERAQHLSHRRRALDNTNSYPDVPDYLALDTN 300
Db 241 TGRGDLATIGHMNPFLLLMATPLERAQHLSHRRRALDNTNSYPDVPDYLALDTN 283
Oy 301 YCFSTEKNCCVRYLYIDFRKDLGKWKIHEPKGYHANFCLGCPYIWSLDTOYSKVLALY 360
Db 284 YCFSTEKNCCVRYLYIDFRKDLGKWKIHEPKGYHANFCLGCPYIWSLDTOYSKVLALY 343
Oy 361 NQHNFGASAAPCCVPOALEPLPIVTVYVGRKPKVEQLSNMIVRSCKS 407
Db 344 NQHNFGASAAPCCVPOALEPLPIVTVYVGRKPKVEQLSNMIVRSCKS 390

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RESULT 5
TGFI_CANFA STANDARD; PRT; 390 AA.
ID TGFI_CANFA
AC P54831;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Transforming growth factor beta 1 precursor (TGF-beta 1).
OS H991.
CN Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [..]
RP SEQUENCE FROM N.A.
RC TISSUE=Jugular vein endothelial;
RX MEDLINE=95237630; PubMed=7721110;
RA Manning A.M., Auchampach J.A., Drong R.F., Slightom J.L.;
RC "Cloning of a canine cDNA homologous to the human transforming growth
NI factor-beta 1-encoding gene.";
HL Gene 155:307-308(1995).
CC -!- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
CC PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
CC HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
CC ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
CC A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC -!- SUBUNIT: Homodimer; disulfide-linked.
CC -!- SIMILARITY: Belongs to the TGF-beta family.
CC -----
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CC -----
CC EMBL: L34956; AAA51458.1; -.
CC PIR: JC4023; JC4023.
CC HSP: P01137; IKLA.
CC InterPro: IPR002400; GF_cysknot.
CC InterPro: IPR003911; TGF_TGFB.
CC InterPro: IPR001839; TGFB.
CC InterPro: IPR001111; TGFB_N.
CC Pfam: PF00019; TGF-beta; 1.
CC Pfam: PF00688; TGFB_propeptide; 1.
CC PRINTS: PR00438; GFCYSKNOT.
CC ProDom: PD000357; TGFB; 1.
CC SMART: SM00204; TGFB; 1.
CC PROSITE: PS00250; TGF_BETA_1; 1.
CC Growth factor; Mitogen; Glycoprotein; Signal.
CC SIGNAL 23 POTENTIAL.
CC FT PROPEP 24 278
CC FT CHAIN 279 390
CC FT DISULFID 285 294
CC FT DISULFID 293 356
CC FT DISULFID 322 387
CC FT DISULFID 326 389
CC FT DISULFID 355 355
CC FT CARBOHYD 82 82
CC FT CARBOHYD 136 136
CC FT CARBOHYD 176 176
CC FT SITE 244 246
CC SEQUENCE 390 AA; 44185 MW; EB4780E88B7B590E CRC64;

Query Match 87.7%; Score 1893.5; DB 1; Length 390;
Best Local Similarity 88.7%; Pred. No. 4.7e-142;
Matches 361; Conservative 12; Mismatches 17; Indels 17; Gaps 1;

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QY 1 MAPSGRLRLPLLLPLLLVLTGPRPAAGLSTCKTIDMELVKRKRIEAIKRLRLA 60
DB 1 MPSPGRLRLPLLLPLLLVLTGPRPAAGLSTCKTIDMELVKRKRIEAIKRLRLS 60
QY 61 SPSPGQDVPGLPLPAVLALYNSTRDRVAGESVEPEPEADYYAKEVTRVLWVSGNQI 120
DB 61 SPSPGQEVPPPLPAVLALYNSTRDRVAGESAEPPEADYYAKEVTRVLWVSGNQI 120
QY 121 YDKFKGTPHSLWMLNTSEIREAVPEPVLSSRAELRLRLKLVQHVLYQKYSNDSWR 180
DB 121 YKVKVKSPIHSIYMLNTSEIREAVPEPVLSSRAELRLRLKLVQHVLYQKYSNDSWR 180
QY 181 YLSNRLAPSDPEMLSFDTGVVQWLTRRAIEGFRLSAHSSSDSKDNTLRVINGFN 240
DB 181 YLSNRLAPSDPEMLSFDTGVVQWLTRRAIEGFRLSAHSSSDSKDNTLRVINGFN 240
QY 241 SGRRGLATIHGMRPFLLLMATPLERAQHLHSSRRRALDNTSYDVPDYASIALDTN 300
DB 241 SSRRGLATIHGMRPFLLLMATPLERAQHLHSSRRRALDNTSYDVPDYASIALDTN 300
QY 301 YCFSTKKNCCVRQLYIDFRKDLGKWKIHEPKGYHANFCLGCPYIWSLDTQYSKVLALY 360
DB 301 YCFSTKKNCCVRQLYIDFRKDLGKWKIHEPKGYHANFCLGCPYIWSLDTQYSKVLALY 360
QY 361 NOHNPASAPCCVPOALEPLPIVYVYVGRKPKVEQLSNMIVRSCKCS 407
DB 361 NOHNPASAPCCVPOALEPLPIVYVYVGRKPKVEQLSNMIVRSCKCS 407
QY 344 NOHNPASAPCCVPOALEPLPIVYVYVGRKPKVEQLSNMIVRSCKCS 390
DB 344 NOHNPASAPCCVPOALEPLPIVYVYVGRKPKVEQLSNMIVRSCKCS 390

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RESULT 6

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TGFI_HORSE
ID TGFI_HORSE STANDARD: PRT: 390 AA.
AC 019011;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Transforming growth factor beta 1 precursor (TGF-beta 1).
GN TGFBI.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph node;
RX MEDLINE=98185507; PubMed=9524819;
RA Penha-Goncalves M.N., Onions D.E., Nicolson L.;
RT "Cloning and sequencing of equine transforming growth factor-beta 1
RT (TGF-beta-1) cDNA."
RL DNA Seq. 7:375-378(1997).
CC -!- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
CC PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
CC HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
CC ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
CC A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC -!- SUBUNIT: Homodimer; disulfide-linked.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the TGF-beta family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X99438; CAA67801.1; -
CC HSSP; P01137; 1KLA
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR003911; TGF-TGFb.
DR InterPro; IPR001839; TGFb.

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DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRINTS; PR01423; TGFbeta.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor; Mitogen; Glycoprotein; Signal.
FT SIGNAL 1 23
FT PROPEP 24 278
FT CHAIN 279 390
FT TRANSFORMING GROWTH FACTOR BETA 1.
FT DISULFID 285 294
FT DISULFID 293 356
FT DISULFID 322 387
FT DISULFID 326 389
FT DISULFID 355 355
FT DISULFID 82 82
FT CARBOHYD 136 136
FT CARBOHYD 176 176
FT SEQUENCE 390 AA; 43974 MW; A86D715F44549691 CRC64;
Query Match 85.2%; Score 1839.5; DB 1; Length 390;
Best Local Similarity 86.5%; Pred. No. 8.6e-138;
Matches 352; Conservative 12; Mismatches 26; Indels 17; Gaps 1;
QY 1 MAPSGRLRLPLLLPLLLVLTGPRPAAGLSTCKTIDMELVKRKRIEAIKRLRLA 60
DB 1 MPSPGRLRLPLLLPLLLVLTGPRPAAGLSTCKTIDMELVKRKRIEAIKRLRLA 60
QY 61 SPSPGQDVPGLPLPAVLALYNSTRDRVAGESVEPEPEADYYAKEVTRVLWVSGNQI 120
DB 61 SPSPGQEVPPGLPLPAVLALYNSTRDRVAGESAETPEPEADYYAKEVTRVLWVSGNQI 120
QY 121 YDKFKGTPHSLWMLNTSEIREAVPEPVLSSRAELRLRLKLVQHVLYQKYSNDSWR 180
DB 121 YKVKVKSPIHSIYMLNTSEIREAVPEPVLSSRAELRLRLKLVQHVLYQKYSNDSWR 180
QY 181 YLSNRLAPSDPEMLSFDTGVVQWLTRRAIEGFRLSAHSSSDSKDNTLRVINGFN 240
DB 181 YLSNRLAPSDPEMLSFDTGVVQWLTRRAIEGFRLSAHSSSDSKDNTLRVINGFN 240
QY 241 SGRRGLATIHGMRPFLLLMATPLERAQHLHSSRRRALDNTSYDVPDYASIALDTN 300
DB 241 SSRRGLATIHGMRPFLLLMATPLERAQHLHSSRRRALDNTSYDVPDYASIALDTN 300
QY 301 YCFSTKKNCCVRQLYIDFRKDLGKWKIHEPKGYHANFCLGCPYIWSLDTQYSKVLALY 360
DB 301 YCFSTKKNCCVRQLYIDFRKDLGKWKIHEPKGYHANFCLGCPYIWSLDTQYSKVLALY 360
QY 361 NOHNPASAPCCVPOALEPLPIVYVYVGRKPKVEQLSNMIVRSCKCS 407
DB 361 NOHNPASAPCCVPOALEPLPIVYVYVGRKPKVEQLSNMIVRSCKCS 407
QY 344 NOHNPASAPCCVPOALEPLPIVYVYVGRKPKVEQLSNMIVRSCKCS 390
DB 344 NOHNPASAPCCVPOALEPLPIVYVYVGRKPKVEQLSNMIVRSCKCS 390

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RESULT 7

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TGFI_MOUSE
ID TGFI_MOUSE STANDARD: PRT: 390 AA.
AC P04202;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Transforming growth factor beta 1 precursor (TGF-beta 1).
GN TGFBI.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86168129; PubMed=3007454;
RA Derynck R., Jarrett J.A., Chen E.Y., Goeddel D.V.;
RT "The murine transforming growth factor-beta precursor."

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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X52498; CAA36741.1; -.
CC PIR: S10219; S10219.
CC HSSP: P01137; IKLA.
CC InterPro: IPR002400; GF_cysknot.
CC InterPro: IPR003911; TGF_TGFB.
CC InterPro: IPR001839; TGFb.
CC InterPro: IPR001111; TGFb_N.
CC Pfam: PF00019; TGF-beta; 1.
CC Pfam: PF00688; TGFb-propeptide; 1.
CC PRINTS: PR00438; GFCYSKNOT.
CC PRINTS: PR01423; TGFbeta.
CC ProDom: PD000357; TGFb; 1.
CC SMART: SM00204; TGFb; 1.
CC PROSITE: PS00250; TGF_BETA_1; 1.
KW Growth factor; Mitogen; Glycoprotein; Signal.
FT SIGNAL 1 23
FT PROPEP 24 278
FT CHAIN 279 390
FT DISULFID 285 294
FT DISULFID 293 356
FT DISULFID 322 387
FT DISULFID 326 389
FT DISULFID 355 355
FT CARBOHYD 82 82
FT CARBOHYD 136 136
FT CARBOHYD 176 176
FT SITE 244 246
SQ SEQUENCE 390 AA; 44329 MW; 5E21108ED50D853C CRG64;

Query Match 85.0%; Score 1835.5; DB 1; Length 390;
Best local Similarity 85.0%; Pred. No. 1.8e-137;
Matches 346; Conservative 14; Mismatches 30; Indels 17; Gaps 1;

QY 1 MAPSGRLRLPLLLPLWLLVLTGPRPAAGLSTCKTIDMELVKKRRTETARGOILSKRLRA 60
DQ 1 MPPSGRLRLPLLLPLWLLVLTGPRPAAGLSTCKTIDMELVKKRRTETARGOILSKRLRA 60
QY 61 SPSSQGDVPGPLPEAVLA-YNSTRDVAGESVEPEPEADYAKETVRLVMVSGNOI 120
DQ 61 SPSSQGEVPGPLPEAVLA-YNSTRDVAGESADPEPEADYAKETVRLVMVDNRNAI 120
QY 121 YDKFKGTPHSLYLFNTSE-REAVPEFVLLSRAELRLKLKVEQHVLYOKYSNDSMR 180
DQ 121 YDKTKDTHSIYFFNTSDIREAVPEPLLSRAELRLQRFKSTVEQHVLYOKYSNNSMR 180
QY 181 YLSNRLAPSDSEWLSEFDTGVVROWLRTREAEGRFSLSAISSDSKONTLHVEINGEN 240
DQ 181 YLGNRLLTPTDPEWLSFDTGVVROWLNGDGIQGRFSAHSCSDSKDNLVHVEINGIS 240
QY 241 SGRAGDLATHICMNRPELL-MATPLERAQHLSSRRRALDNTSYDPDVAASLALDNT 300
DQ 241 PKRGDLGTHDMNRPELL-MATPLERAQHLSSRRR-----ALDNTN 283
QY 301 YCFSTSEKNCVRLQYIDFKNGLGWKWIHEPKGYHANFCLGCPYIWSLDTQYSKVLALY 360
DQ 284 YCFSTSEKNCVRLQYIDFKNGLGWKWIHEPKGYHANFCLGCPYIWSLDTQYSKVLALY 343
QY 361 NQHPGASAPCCVPALEPLPIYVYVGRKPKVEQLSNMIVRSCKS 407
DQ 344 NQHPGASAPCCVPALEPLPIYVYVGRKPKVEQLSNMIVRSCKS 390

RESULT 9
TGFL_CAVPO STANDARD; PRT; 390 AA.
ID Q92L1Y6; Q92B3; Q9R148;
AC 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Transforming growth factor beta 1 precursor (TGF-beta 1).
GN TGFBI.

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OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_taxonomy:10141;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN-Hartley;
RA Jeevan A., McMurray D.N., Yoshimura T.;
RT *Guinea pig transforming growth factor-beta in peritoneal exudates
RT after BCG vaccination.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RN SEQUENCE OF 265-382 FROM N.A.
RX MEDLINE-99144670; PubMed-10025978;
RA Scarozza A.M., Ramsingh A.L., Wicher V., Wicher K.;
RT "Spontaneous cytokine gene expression in normal guinea pig blood and
RT tissues.";
RL Cytokine 10:851-859(1998).
RN [3]
RN SEQUENCE OF 279-371 FROM N.A.
RC STRAIN-Hartley; ISSUE-Trachea;
RA Morishima Y., Uchida Y., Nomura A., Ishii Y., Sakamoto T.,
RA Sekizawa K.;
RT *Guinea-pig transforming growth factor-beta expression in injured
RT tracheal epithelium";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: MULTIFUNCTIONAL PEPTIDE THAT CONTROLS PROLIFERATION,
CC DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL TYPES. MANY
CC CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF THEM HAVE
CC SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1 REGULATES THE
CC ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES A
CC POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the TGF-beta family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF191297; AAF02780.1; -.
CC EMBL: AF097509; AAC83807.1; -.
CC EMBL: AF169347; AAD49347.1; -.
CC HSSP: P01137; IKLA.
CC InterPro: IPR002400; GF_cysknot.
CC InterPro: IPR003911; TGF_TGFB.
CC InterPro: IPR001839; TGFb.
CC InterPro: IPR001111; TGFb_N.
CC Pfam: PF00019; TGF-beta; 1.
CC Pfam: PF00688; TGFb-propeptide; 1.
CC PRINTS: PR00438; GFCYSKNOT.
CC PRINTS: PR01423; TGFbeta.
CC ProDom: PD000357; TGFb; 1.
CC SMART: SM00204; TGFb; 1.
CC PROSITE: PS00250; TGF_BETA_1; 1.
KW Growth factor; Mitogen; Glycoprotein; Signal.
FT SIGNAL 1 24
FT PROPEP 25 278
FT CHAIN 279 390
FT DISULFID 285 294
FT DISULFID 293 356
FT DISULFID 322 387
FT DISULFID 326 389
FT DISULFID 355 355
FT CARBOHYD 82 82
FT CARBOHYD 136 136
FT CARBOHYD 176 176
FT SITE 244 246
FT CONFLICT 279 279

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FT CONFLICT 286 286 F -> S (IN REF. 2).
FT CONFLICT 309 309 K -> E (IN REF. 2).
FT CONFLICT 322 322 C -> R (IN REF. 2).
FT CONFLICT 350 350 A -> G (IN REF. 2).
SQ SEQUENCE 390 AA: 44328 MW: 1539F849BA0C0FF1 CRC64;

Query Match 84.6%; Score 1826.5; DB 1; Length 390;
Best Local Similarity 84.8%; Pred. No. 9.2e-137; Indels 17; Gaps 1;
Matches 345; Conservative 15; Mismatches 30;

Qy 1 MAPSGRLPLPLLLPLMLVLTGPRPAAGLSTCKTIDMELVKRRIRIAIRGOILSKRLA 60
Db 1 MPPSRLLPLPLLLPLMLVLTGPRPAAGLSTCKTIDMELVKRRIRIAIRGOILSKRLA 60
Qy 61 SPPSQGDVPPGCPLEAVLALYNSTRDRVAGSEPEPEPEADYAKVETRLVMESGNOI 120
Db 61 SPPSQGDVPPGCPLEAVLALYNSTRDRVAGSEPEPEPEADYAKVETRLVMESGNOI 120
Qy 121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLRLKLVQHVLYQKYSNDSWR 180
Db 121 YKSIETVAHSIYMFNTSELREAVPDPLLSRAELRWORLKNVQHVLYQKYSNDSWR 180
Qy 181 YLSNKLAPSDSEPLSFVDTGVVQWLTREALEGFRLSAHSSSDSKDNTLHVEINGFN 240
Db 181 YLSNQLTPTDPEWLSFDVTGVVQWLTREALEGFRLSAHSSSDSKDNTLHVEINGFN 240
Qy 241 SGRGOLATIHGMNRPFLMATPLERAOHLHSSRRHREALDTNSYPDVPDYASALDTN 300
Db 241 PKRGDLAAIHGMNRPFLMATPLERAOHLHSSRRHREALDTNSYPDVPDYASALDTN 300
Qy 301 YCFSTERNKCCVRLQYIDFRDLGKWKIHEPKGYHANFCLGCPYIWSLDTQYSKVLA 360
Db 301 YCFSTERNKCCVRLQYIDFRDLGKWKIHEPKGYHANFCLGCPYIWSLDTQYSKVLA 360
Qy 361 NOHNPASAAAPCCVQALPEPIVYVGRKPKVEQLSNMIVRSCKS 407
Db 344 NOHNPASAAAPCCVQALPEPIVYVGRKPKVEQLSNMIVRSCKS 390

RESULT 10
TGFL_BOVIN STANDARD; PRT: 315 AA.
AC P18341;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Transforming growth factor beta 1 precursor (TGF-beta 1) (Fragment).
GN TGFBI.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91042552; PubMed=3133459;
RA van Obergheon-Schilling E., Kondalah P., Ludwig R.L., Sporn M.B.,
RA Baker C.C.;
RT "Complementary deoxyribonucleic acid cloning of bovine transforming
RT growth factor-beta 1."
RL Mol. Endocrinol. 1:693-698(1987).
RN [2]
RP SUBUNITS.
RC TISSUE=Bone;
RX MEDLINE=92129307; PubMed=1733936;
RA Ogawa Y., Schmidt D.K., Dasch J.R., Chang R.J., Glaser C.B.;
RA "Purification and characterization of transforming growth factor-beta
RT 2.3 and -beta 1.2 heterodimers from bovine bone."
RL J. Biol. Chem. 267:2325-2328(1992).
CC -1- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
CC PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
CC HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
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CC ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
CC A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC -1- SUBUNIT: Homodimer; disulfide-linked. Heterodimers of TGF-beta 1/2
CC have been found in bone.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the TGF-beta family.
CC
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CC
CC ENBL; M36271; AAA30778.1; .
CC PIR; A40057; A40057.
CC HSP; P01137; 1KLA.
CC InterPro: IPR002400; GF_cysknot.
CC InterPro: IPR003911; TGF_TGFB.
CC InterPro: IPR001839; TGFB.
CC InterPro: IPR001111; TGFB_N.
CC Pfam: PF00019; TGF-beta; 1.
CC Pfam: PF00688; TGFB_propeptide; 1.
CC PRINTS; PR00438; GFCYSKNOT.
CC PRINTS; PR01423; TGFBETA.
CC PRODOM; PD000357; TGFB; 1.
CC SMART; SM00204; TGFB; 1.
CC PROSITE; PS00250; TGF_BETA_1; 1.
CC Growth factor: Mitogen; Glycoprotein.
CC FT NON_TER 1 1
CC FT PROPEP <1 203
CC FT CHAIN 204 315 TRANSFORMING GROWTH FACTOR BETA 1.
CC FT DISULFID 210 219 BY SIMILARITY.
CC FT DISULFID 218 281 BY SIMILARITY.
CC FT DISULFID 247 312 BY SIMILARITY.
CC FT DISULFID 251 314 BY SIMILARITY.
CC FT DISULFID 280 280 INTERCHAIN (BY SIMILARITY).
CC FT CARBOHYD 7 7 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT SITE 169 171 CELL ATTACHMENT SITE (POTENTIAL).
CC SQ SEQUENCE 315 AA; 36269 MW; C2717A23D94E00E CRC64;

Query Match 72.8%; Score 1572.5; DB 1; Length 315;
Best Local Similarity 88.9%; Pred. No. 7.6e-117; Indels 17; Gaps 1;
Matches 295; Conservative 9; Mismatches 11;

Qy 76 AVLALYNSTRDRVAGESVEPEPEADYAKVETRLVMESGNOIYDKFKGTPHSLYMLF 135
Db 1 AILALYNSTRDRVAGESAETEPEPEADYAKVETRLVMVEYGNKIYDKMKSSHSITMFF 60
Qy 136 NSELRAVPEPVLLSRAELRLRLKLVQHVLYQKYSNDSWRYLSNKLAPSDSPW 195
Db 61 NSELRAVPEPVLLSRAELRLRLKLVQHVLYQKYSNDSWRYLSNKLAPSDSPW 120
Qy 196 LSFDTGVVQWLTREALEGFRLSAHSSSDSKDNTLHVEINGFSGRRGLATIHGMNR 255
Db 12 LSFDTGVVQWLTREALEGFRLSAHSSSDSKDNTLHVEINGFSGRRGLATIHGMNR 180
Qy 256 PFLLMATPLERAOHLHSSRRHREALDTNSYPDVPDYASALDTNYCFSTERNKCCVRL 315
Db 181 PFLLMATPLERAOHLHSSRRHREALDTNSYPDVPDYASALDTNYCFSTERNKCCVRL 223
Qy 316 YIDFKDLGKWKIHEPKGYHANFCLGCPYIWSLDTQYSKVLAALYNQHNPGASAPCCVP 375
Db 224 YIDFKDLGKWKIHEPKGYHANFCLGCPYIWSLDTQYSKVLAALYNQHNPGASAPCCVP 283
Qy 376 QALEPLPIVYVGRKPKVEQLSNMIVRSCKS 407
Db 284 QALEPLPIVYVGRKPKVEQLSNMIVRSCKS 315
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RESULT 11
TGFL_CHICK
ID TGFL_CHICK STANDARD; PRT; 373 AA.
AC P09531;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Transforming growth factor beta 1 precursor (TGF-beta 1) (TGF-beta 4)
DE (Fragment).
GN TGFB1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OC NCBI_TaxID=9031;
RX [1]
SEQUENCE FROM N.A.
RC STRAIN=White Leghorn;
RX MEDLINE=89112198; PubMed=2464131;
RA Jakowlew S.B., Dillard P.J., Sporn M.B., Roberts A.B.;
RT "Complementary deoxyribonucleic acid cloning of a messenger
RT ribonucleic acid encoding transforming growth factor beta 4 from
RT chicken embryo chondrocytes.";
RL Mol. Endocrinol. 2:1186-1195(1988).
RN [2]
REVISONS.
RX MEDLINE=92357039; PubMed=1355860;
RA Burt D.W., Jakowlew S.B.;
RT "Correction: a new interpretation of a chicken transforming growth
RT factor-beta 4 complementary DNA.";
RL Mol. Endocrinol. 6:989-992(1992).
CC -1- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
CC PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
CC HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
CC ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
CC A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC -1- SUBUNIT: Homodimer; disulfide-linked.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the TGF-beta family.
CC
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CC or send an email to license@sb-sib.ch).
CC
CC EMBL; M31160; AAB05637.1; .
CC PIR; A41918; A41918.
CC HSSP; P01137; 1KLA.
CC InterPro; IPR003911; TGF_TGFB.
CC InterPro; IPR001839; TGFB.
CC InterPro; IPR001111; TGFB_N.
CC Pfam; PF00019; TGF-beta; 1.
CC Pfam; PF00688; TGFB_propeptide; 1.
CC PRINTS; PR01423; TGF-BETA.
CC ProDom; PD000357; TGFB; 1.
CC SMART; SM00204; TGFB; 1.
CC PROSITE; PS00250; TGF_BETA_1.
CC Growth factor; Mitogen; Glycoprotein; Signal.
CC NON_TER 1 1
CC SIGNAL <1 1 POTENTIAL.
CC PROPEP 2 259 POTENTIAL.
CC CHAIN 260 373 TRANSFORMING GROWTH FACTOR BETA 1.
CC FT DISULFID 266 277 BY SIMILARITY.
CC FT DISULFID 276 339 BY SIMILARITY.
CC FT DISULFID 305 370 BY SIMILARITY.
CC FT DISULFID 309 372 BY SIMILARITY.
CC FT DISULFID 338 338 INTERCHAIN (BY SIMILARITY).
CC FT CARBOHYD 54 54 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).
```

```
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SITE 224 226 CELL ATTACHMENT SITE (POTENTIAL).
SQ SEQUENCE 373 AA; 42634 MW; 9903F3479C8552E5 CRC64;

Query Match 48.5%; Score 1047; DB 1; Length 373;
Best Local Similarity 52.9%; Pred. No. 2.9e-75;
Matches 207; Conservative 52; Mismatches 100; Indels 32; Gaps 8;

Qy 30 ISTCKTDMELVKKRRIEATNGQLLSKRLASPPSQDPPGPIIPAYLALYNSTRDVA 89
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 2 ISTQRDLLEAAKKKRIEAVRGQILSLRTAPPASETPPRLPDVDRALYNSTQELK 61
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Qy 90 GES-VEPEPEADYAYAKEVTRVLWVESGNOIQDKFKGTPHSLYMLFNTSELREAVPEV 148
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 62 QRARLRPPDPGPDYNAKELRIPMETTWGAEHWQPSHSIFFVFNVSRRRG-GRPT 120
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Qy 149 LLSRAELRLRLKLLK-----VEQHVELYQKYSNDWSRYLSNRLAPSDSPESLFDVTGV 203
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 121 LLHRAELRLRQKAADSAGTEQRLELYQGYGNASRYLHGKSVRATADDEWLSFDVDA 180
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Qy 204 VRQMLTRREALIEGRLSAHSSD---SKDNTLHVEINGFNSGRGDLATIGHNRR--PFL 258
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 181 VHQWLSGSELLGVFKLSVHCPCMGPGHAEPMRTISIEGFEQ-ORGDHQSTAKKRRVPYV 239
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Qy 259 LLMATPLERAQHLHSSRRRALDNTSYDPDYPDVASLALDNTYCF---SSTEKNCCVRQLY 316
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 240 LAMA:PAFRANFLHSAHRR-----DLDDYCFGPGCTDEKNCCVRPLY 282
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Qy 317 IDFRKDLGWKWIHEPKGYHANFCLGPGCPYIWSLDTQYSKVLALYNQHNPGASAPCCVPQ 376
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 283 IDFRKDLGWKWIHEPKGYMANFCMPCPYIWSADTQYTKVLALYNQHNPGASAPCCVPQ 342
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Qy 377 ALEPLPYVYVYGRKPKVEQLSNMIVRSCKS 407
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 343 TLDPLPIIYVYGRNVRVEQLSNMIVRSCKS 373

RESULT 12
TGFL_XENLA
ID TGFL_XENLA STANDARD; PRT; 382 AA.
AC P16176;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Transforming growth factor beta 1 precursor (TGF-beta 1) (TGF-beta 5).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
OC Xenopodinae; Xenopus.
OC NCBI_TaxID=8355;
RX [1]
SEQUENCE FROM N.A.
RX MEDLINE=90110090; PubMed=2295601;
RA Kondaiah P., Sands M.J., Smith J.M., Fields A., Roberts A.B.,
RA Sporn M.B., Melton D.A.;
RT "Identification of a novel transforming growth factor-beta (TGF-beta
RT 5) mRNA in Xenopus laevis.";
RL J. Biol. Chem. 265:1089-1093(1990).
RN [2]
SEQUENCE FROM N.A.
RA Vempati U.D., Kondaiah P.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: IMPORTANT ROLE IN CERTAIN ASPECTS OF DIFFERENTIATION.
CC -1- SUBUNIT: Homodimer; disulfide-linked.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the TGF-beta family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@sb-sib.ch).
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or send an email to license@lsb-sib.ch).
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CC EMBL: J05180; AAA49968.1; -.
CC EMBL: AF009335; AAB64441.1; -.
CC EMBL: AF009331; AAB64441.1; JOINED.
CC EMBL: AF009332; AAB64441.1; JOINED.
CC EMBL: AF009333; AAB64441.1; JOINED.
CC EMBL: AF009334; AAB64441.1; JOINED.
CC PIR: A34229; B61036.
CC HSSP: P01137; IKLA.
CC InterPro: IPR002400; GF_cysknot.
CC InterPro: IPR003911; TGF_TGFB.
CC InterPro: IPR001839; TGFB.
CC InterPro: IPR001111; TGFB_N.
CC Pfam: PF00019; TGF-beta; 1.
CC Pfam: PF00688; TGF-beta; 1.
CC PRINTS: PR00438; GFCYSKNOT.
CC PRINTS: PR01423; TGFBETA.
CC PRODOM: PD000357; TGFB; 1.
CC SMART: SM00204; TGFB; 1.
CC PROSITE: PS00250; TGF_BETA_1; 1.
KW Growth factor; Mitogen; Glycoprotein; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT PROPEP 22 270
FT CHAIN 271 382
FT DISULFID 277 286
FT DISULFID 285 348
FT DISULFID 314 379
FT DISULFID 318 381
FT DISULFID 347 381
FT CARBOHYD 73 73
FT CARBOHYD 123 123
FT CARBOHYD 166 166
FT SITE 234 236
SQ SEQUENCE 382 AA; 44200 MW; 1034621C517AAE15 CRC64;

Query Match
Best Local Similarity 40.2%; Score 868.5; DB 1; Length 382;
Matches 190; Conservative 55; Mismatches 62; Indels 47; Gaps 11;

QY 9 LPLLPLMLLVLPGRPAAGLSCTCKIDMELVYKRIEIRGILSKRLASPPSGDV 68
DB 1 MEVLMLLVLLVLSLAMSLSCTKAVDMEEVYKRIEIRGILSKRLDTPDV-DS 59
QY 69 PPGPLPAVLALYNSTRDEAVAGESVEPE-----PEPEADYVYKVTYVLMVESCNOIYDK 123
DB 60 EKMTVPSEAFILYNSTLTVIREKATREEHVGHQDQIYAKQYR---FESITELED- 115
QY 124 FKGTPLSLYMLFNTSELREAVPEVPLSRABELRLRLKL--KVPQHVLYKYKYSNDGW-- 179
DB 116 -----HEFKFNASHVRENYGMNSLLHHAELRYKKQTKNMDDQRMELFWKYQENGTH 170
QY 180 -RILSNRLAPSDSPLEWLEFDVTGVVRQWLTRREAIEGERLSAH---SSSDSKDNTLIVE 235
DB 171 SRYLESKYITPTDDEWMSFDVTGVVNLKRAENEFQGLQPACKPTPOAKD-----ID 226
QY 236 INFGNSRRGRDLATIGHM--NRPELLLMATPLERAQHLHSSRRRLDNTSNYPYDVPDYA 293
DB 227 IEGF-PALRGDLASLSKENTKPYLMITSMPAERIDVTSSKKR----- 270
QY 294 SLALDNTYCFSTKNCVROLYIDFRKDLGKWKIHEPKGYHANFCGLGPCPIYWSLDTQY 353
DB 271 --GVQYECFGNGNPGCKVPIYFRKDLGKWKIHEPKGYEANYCLGNCPIYWSMDTQY 328
QY 354 SKVLALYNQHPGASAPCCVPQALEPLPIYVYVGRPKVQOLSNMIVRSCKCS 407
DB 329 SKVLSLYNQNPNGASIPCCVPDVLPLEPIIYVYVGRTAKEVQLSNMIVRSNCSS 382

RESULT 13
TGF3_CHECK
ID TGF3_CHECK
AC P16047;
```



```

Chen E.Y.;
EMBO J. 7:3737-3743(1988).
-|- FUNCTION: INVOLVED IN EMBRYOGENESIS AND CELL DIFFERENTIATION.
-|- SUBUNIT: Homodimer; disulfide-linked.
-|- SUBCELLULAR LOCATION: Secreted.
-|- SIMILARITY: belongs to the TGF-beta family.
-----
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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EMBL; X14150; CAA32363.1; .
PIR; S01825; S01825.
HSP; P10600; 1TGJ.
InterPro: IPR002400; GF_cysknot.
InterPro: IPR003911; TGF-TGFB.
InterPro: IPR001839; TGFB.
InterPro: IPR001111; TGFB_N.
Pfam: PF00019; TGF-beta; 1.
Pfam: PF00688; TGFB_propeptide; 1.
PRINTS; PR00438; GFGYSKNOT.
PRINTS; PR01423; TGBETA.
ProDom; PD000357; TGFB; 1.
SMART; SM00204; TGFB; 1.
PROSITE; PS00250; TGF_BETA_1; 1.
Growth factor: Mitogen; Glycoprotein; Signal.
POTENTIAL..
FT SIGNAL 1 18
FT PROPEP 19 297
FT CHAIN 298 409
FT DISULFID 304 313
FT DISULFID 312 375
FT DISULFID 341 406
FT DISULFID 345 408
FT DISULFID 374 374
FT CARBOHYD 72 72
FT CARBOHYD 133 133
FT CARBOHYD 140 140
FT SITE 259 261
SQ SEQUENCE 409 AA; 46814 MW; B4900235B5C955E CRC64;
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Query Match 38.6%; Score 834; DB 1; Length 409;
Best Local Similarity 44.6%; Pred No. 2.le-58;
Matches 190; Conservative 58; Mismatches 122; Indels 56; Gaps 14
Oy 15 LILWLVLTGPRPAAGLSTCKTIDMELVKRKRIEFAIRGOILSKURLASPPSGQVPPGPP 74
Db 7 LVYALLNFATVSLMSCTCTIDFDHKRKREVAIRGOILSKURLASPPDSML--ANIP 64

```

[illegible]

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OM protein - protein search, using sw model

Run on: October 7, 2003 17:58:47 ; Search time 99 Seconds
(without alignments)
1060.883 Million cell updates/sec

Title: US-10-017-372E-37

Perfect score: 2159

Sequence: 1 MAPSGLRLPLLLPLMLLV.....GRKPVEQLSNMIVRSCKS 407

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organalle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteria2:*

17: sp_archaea2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1815.5	84.1	390	Q9TUM8	Q9TUM8 equus caball
2	1736.5	80.4	368	Q8K4D9	Q8K4D9 sigmodon hi
3	849.5	39.3	379	Q8JHF5	Q8JHF5 sparus aura
4	845.5	39.2	379	Q8AXK8	Q8AXK8 sparus aura
5	827.5	38.3	412	Q1YU7	Q1YU7 mus musculus
6	825	38.2	382	Q9PWA9	Q9PWA9 morone chry
7	821	38.0	414	Q91VP5	Q91VP5 mus musculus
8	806	37.3	382	Q93449	Q93449 oncorhynch
9	780	36.1	376	Q9PT02	Q9PT02 cyprinus ca
10	760	35.2	399	Q9ERB7	Q9ERB7 mesocricetu
11	719.5	33.3	362	Q99K17	Q99K17 mus musculus
12	691.5	32.0	130	Q08714	Q08714 mesocricetu
13	674.5	31.2	124	Q95N80	Q95N80 canis fami
14	673.5	31.2	361	Q98854	Q98854 cyprinus ca
15	638	29.6	112	Q02730	Q02730 oryctolagus
16	600	27.8	255	Q921T1	Q921T1 mus musculus

ALIGNMENTS

RESULT 1

Q9TUM8

ID Q9TUM8 PRELIMINARY; PRT: 390 AA.

AC Q9TUM8; SEQUENCE FROM N.A.

DT 01-MAY-2000 (TREMHLrel. 13, Created)

DT 01-MAY-2000 (TREMHLrel. 13, Last sequence update)

DE 01-MAR-2003 (TREMHLrel. 23, Last annotation update)

DE Transforming growth factor beta 1.

GN TGFBI.

OS Equus caballus (Horse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

OX NCBI_TaxID-9796;

RN [1]

RP SEQUENCE FROM N.A.

RA Nixon A.J., Brower-Toland B.T., Sandell L.J.;

RI "Molecular cloning of equine transforming growth factor beta 1 reveals

a divergent nucleotide structure that encodes a novel bioactive

peptide among mammalian species.";

RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

DR EMBL: AF175709; AND49431.1; -

DR HSSP: P01137; IKLA.

DR InterPro: IPR002400; GF_cysknot.

DR InterPro: IPR001839; TGFb.

DR InterPro: IPR001111; TGFb.N.

DR InterPro: IPR003911; TGF-TGFb.

DR Pfam: PF00019; TGF-beta; 1.

DR Pfam: PF00688; TGFb_propeptide; 1.

DR PRINTS: PR01423; TGFbETA.

DR PRODOM: PD000357; TGFb; 1.

DR SMART: SM00284; TGFb; 1.

DR PROSITE: PS00250; TGF-BETA_1; 1.

SQ SEQUENCE 390 AA; 43860 MW; 220FE40DFCCA6016 CRC64;

Query Match

Best Local Similarity 84.1%; Score 1815.5; DB 6; Length 390;

Matches 348; Conservative 12; Mismatches 30; Indels 17; Gaps 1;

Q9TUV8 canis fami
Q8CDZ9 mus musculu
Q90VF1 pleuronecte
Q9R184 meriones un
Q90VF2 pleuronecte
Q90VF5 pleuronecte
Q90Y17 oncorhynch
Q90ZE7 acipenser b
Q42306 carassius a
Q9MY21 capra hircu
Q82K41 cervus elap
Q8WV88 homo sapien
Q9NLS3 capreolus c
Q8UWD8 columba liv
Q8AVB2 coturnix co
Q8UWD7 coturnix ch
Q90YV0 ictalurus p
Q8JHB6 scophthalmu
Q90YF8 oncorhynch
Q98SP0 gallus gall
Q9GM97 equus cabal
Q8UWD9 anas platyr
Q8HY52 lepus capen
Q95J86 macaca fasc
Q28240 cervus elap
Q90ZJ7 anguilla an
Q90VF4 pleuronecte
Q8WNS6 bos taurus

17 584.5 27.1 127 6 Q9TUV8
18 570 26.4 224 11 Q8CDZ9
19 561.5 26.0 200 13 Q90VF1
20 554 25.7 101 11 Q9R184
21 456 21.1 179 13 Q90VF2
22 433 19.1 68 13 Q90VF5
23 402 18.6 88 13 Q90Y17
24 397 18.4 88 13 Q90ZE7
25 393 18.2 87 13 Q42306
26 383 17.7 91 6 Q9MY21
27 373 17.3 86 6 Q82K41
28 371.5 17.2 309 4 Q8WV88
29 358 16.6 81 6 Q9NLS3
30 336.5 15.6 375 13 Q8UWD8
31 323.5 15.0 375 13 Q8AVB2
32 321.5 14.9 375 13 Q8UWD7
33 321.5 14.9 389 13 Q90YV0
34 320 14.8 87 13 Q8JHB6
35 317 14.7 77 13 Q90YF8
36 316.5 14.5 375 13 Q98SP0
37 313.5 14.5 375 6 Q9GM97
38 313.5 14.5 375 13 Q8UWD9
39 311.5 14.4 375 13 Q8UWD9
40 309.5 14.3 375 6 Q8HY52
41 306.5 14.2 375 6 Q95J86
42 302 14.0 50 6 Q28240
43 301 13.9 62 13 Q90ZJ7
44 300 13.9 62 13 Q90VF4
45 296.5 13.7 375 6 Q8WNS6

```

DR InterPro: IPR001839; TGFb.
DR InterPro: IPR001111; TGFb_N.
DR InterPro: IPR003911; TGF-TCFb.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGFb.propeptide; 1.
DR PRINTS: PR01423; TGFbETA.
DR PRODOM: PD000357; TGFb; 1.
DR SMART: SM00204; TGFb; 1.
DR PROSITE: PS00250; TGF_BETA_1; 1.
KW Growth factor; Mitogen; Glycoprotein; Signal.
FT SIGNAL 1 22
FT PROPEP 23 264
FT CHAIN 265 376
FT DISULFID 272 280
FT DISULFID 308 373
FT DISULFID 312 375
FT DISULFID 341 341
FT CARBOHYD 76 76
FT CARBOHYD 125 125
FT CARBOHYD 167 167
FT SITE 230 232
FT SEQUENCE 376 AA; 43329 MW; 7E7FC4DA58B69681 CRC64;

Query Match 36.1%; Score 780; DB 13; Length 376;
Best Local Similarity 43.6%; Pred. No. 2.6e-60;
Matches 179; Conservative 64; Mismatches 122; Indels 46; Gaps 15;

QY 6 LRLPLLLPILLLVLTGPRPAAGLSTCKTIDMELVKKRIEIRGQILSKRLASPPSQ 65
DB 1 MRVSELLALQCLGFV--HYSGALSTCSPDLDELKKRIEIRGQILSKRLSKEPEV 58

QY 66 GVPPEP-LPEAVLALYNST---RDRVAGESVEPEPEP-EADYYAKEVTR--VLMVSEGN 118
DB 59 DEEKESQNPAPLISVYNSTVELNEQAPPEQKEDPVEEYAKEVHKFTIKLMKNP 118

QY 119 QIYDFEKTGSHLYMLFNTSELREAVPEPVLSSRAELRLRLK--VEOHVELYQKYSN 176
DB 119 ---DKF-----LWFNIIDISQTLNRIISQVELRLLLITTPDGSQERLELYQVIGN 167

QY 177 DSWRYLSNRLAPSDSPFWLTFDVTGVVROWLTRREAEIGFRLSAHSSDSKDNLTLYVEI 236
DB 168 KS-RYLSRFI--PNQKWLSPDVTQTLKDWLQSEAEQGLKWNADCDPO-KTFQLKI 223

QY 237 NGFNSGRGDLATII-GNNEPELLMATPLERAQHLHSSRRRALDNTSNYPDYPDASL 295
DB 224 PGLVL-VRGDTETLAVNMPPEHLYMSPLD--GNNSKSRKRROTETDQVCTDKSD---- 277

QY 296 ALDNTYCSSTKNCVRLYIDFRKDLGKWIHEPKGVHNEFLGPGCPYIWSLDTQYSK 355
DB 278 -----GCCVRSLYIDFRKDLGKWIHEPKGVHNEFLGPGCPYIWSLDTQYSK 324

QY 356 VLALYNQHNPGASAPCCVPOALEPLPIVYVGRPKVQQLSNMIVRSCKC 406
DB 325 VLALYKHNPGASAPCRVQVNLNPLPIFYVYVGRQHKVQQLSNMIVKTKC 375

RESULT 10
Q9ERB7 PRELIMINARY; PRT; 399 AA.
AC Q9ERB7
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE Transforming growth factor-beta 2 (Fragment).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RA Ramesh G., Kondaliah P., Seshagiri P.B.;
RT "Differential expression and selective localization of transforming
growth factor-beta isoforms in the hamster uterus during estrous
cycle.";
RT Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL: AY007214; AAC02247.1; -.
DR HSSP: P08112; 2TGI.
DR InterPro: IPR001839; TGFb.
DR InterPro: IPR001111; TGFb_N.
DR InterPro: IPR003911; TGF-TCFb.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGFb.propeptide; 1.
DR PRINTS: PR01423; TGFbETA.
DR PRODOM: PD000357; TGFb; 1.
DR SMART: SM00204; TGFb; 1.
DR PROSITE: PS00250; TGF_BETA_1; 1.
FT NON_TER 1 399
FT NON_TER 1 399
FT SEQUENCE 399 AA; 46078 MW; A6FF8E65EAFD5148 CRC64;

Query Match 35.2%; Score 760; DB 11; Length 399;
Best Local Similarity 42.1%; Pred. No. 1.7e-58;
Matches 177; Conservative 59; Mismatches 122; Indels 62; Gaps 15;

QY 18 LVLTPGRPAAGLSTCKTIDMELVKKRIEIRGQILSKRLASPPSGDVP-PGPLPEA 76
DB 4 LLHLVP--VALSUSTCTLDMDQFMRAIRIEAIRGQILSKRLKLTSPPE--DYPEPEVPE 59

QY 77 VLALYNSTRD---RVAGESVEPEPE-PEADYYAKEVTRVLM---VESGNOIYDKFKGTP 128
DB 60 VISIYNSTRDLLQEKASRRAAACERESDEEYAKEVYKIDMPSPFSENAIPPTFY-RP 118

QY 129 HSLVMLNTSELREAVPEPVLSSRAELRLRL---KLKV-EQHVVELYQ-----KYSNDSW 179
DB 119 YFRIVRFVDVSMMEKNASN--LVKAEFRVFLQPKARVAEQRIELYQILKSKDLTSPTQ 175

QY 180 RYLSNRLAPSDSPFWLTFDVTGVVROWLTRREAEIGFRLSAH-----SSSDSK 228
DB 176 RYDSQVYKVTAEGLWSLFDVDAVHEWLHKKRNGLFKISLHCPCTFFVFNNTIIPNK 235

QY 229 DNTLHVE---INGNSGRGDLATIHGMNR-----PFLIMATPLERAQHLHSSRRRA 279
DB 236 SEELEAFAGIDGTQSHSSGHOETIKSTRKNSCKTPELLMLLPSYRLESQSNRRKKR 295

QY 280 LDTNSYPDYPDASLALDNTYCSSTKNCVRLYIDFRKDLGKWIHEPKGVHNEFLGPGCPYI 339
DB 296 -----ALDAAVCFPNVDNCCRLPLYIDFRKDLGKWIHEPKGVHNEFLGPGCPYI 339

QY 340 LGPCPYIWSLDTQYSKVLALYNQHNPGASAPCCVPOALEPLPIVYVGRPKVQQLSNM 399
DB 340 AGACPYLWSSDTQHTKVLISLNTINPEASAPCCVSHDLEPLTILYIGNTPKIEQLSNM 399

RESULT 11
Q99K17 PRELIMINARY; PRT; 362 AA.
AC Q99K17
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Similar to transforming growth factor, beta 3 (Fragment).
GN TGFb3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RA Strausberg R.;
RA Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL: BC005513; AAH05513.1; -.
DR HSSP: P10600; 1TGI.
DR MGD; MGI:98727; Tgfb3.

```

InterPro: IPR002400; GF_cysknot.
DR InterPro: IPR001839; TGFb.
DR InterPro: IPR001111; TGFb_N.
DR InterPro: IPR003911; TGF_TGFb.
DR Pfam: PF00019; TGF-beta_1.
DR Pfam: PF00688; TGFb_propeptide; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PRINTS: PR01423; TGFbETA.
DR ProDom: PD000357; TGFb; 1.
DR SMART: SM00204; TGFb; 1.
DR SMART: SM00250; TGF_BETA_1; 1.
DR NON_TER 1
FT SEQUENCE 362 AA; 41486 MW; 0808E46180FADAE70 CRC64;
SQ

Query Match 33.3%; Score 719.5; DB 11; Length 362;
Best Local Similarity 42.9%; Pred. No. 5.4e-55;
Matches 164; Conservative 51; Mismatches 114; Indels 53; Gaps 13;

QY 58 RLASPPSQGDVPPGLPEAVIALYANSTR---DRVAGESVE--PEPEADYAKEVTRVL 112
DB 2 RVGSPEPSVMT--HVPYVLYALYNSTRLEELHEHGEREGCTQETSESEYAKEIHKFD 59
QY 113 MYE---SGNQIYDKPGPHSYLMFNTSELREAVPEVPLLSRAELRLRL----KLKVE 165
DB 60 MIQGLAEHVELAVCPKGIITSKVR-FNYSVSEK---NGTNLFRAEFRLVRPNPSSKRT 115
QY 166 QVVELYQKYSND----SWRLSNRLLASDPSEWLSFDVTGVVQWLTTRRAIEGFRLSA 221
DB 116 QRIELFOILRPDEHIAKQYIGGNLPTGTAEWLSFDVDTVREWLRLRESNGLGLSIS 175
QY 222 H-----SSDSOKN---TLHVEINGNS---GRRGDLATHGM---NRPELLMATPL 265
DB 176 HCPCHTFQPNQDILENVEHWEIKEFGVDNEDHGRLKKGOKDHNPHLILMIPP 235
QY 266 ERAQHLHSHRRRALDTNSYPDVPDYASLALDTNYCFSTKNCVROLYIDFRKDLGW 325
DB 236 HRLDSPGQSQRK-----KRALDTNYCFRNLEENCCVRLPYIDFRQDLGW 280
QY 326 KWIHEPKGYHANFCIGPCPYIWSLDTQYSKVLALYNQHNPGASAPCCVPOALEPLPIY 385
DB 281 KWIHEPKGYANFCSPCLYASADTHTSTVLGLYNTLNPEASAPCCVPODLEPLTILY 340
QY 386 YVGRKPKVEQLSNMIVRS-KCS 407
DB 341 YVGRTPKVEQLSNMIVRS-KCS 362

RESULT 12
Q08714
ID Q08714 PRELIMINARY; PRT; 130 AA.
AC Q08714; 070331.
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Transforming growth factor beta 1 (TGF-beta 1) (Fragment).
GN TGFb1.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OC NCBI_TaxID=10036;
OX [1]
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LVG (SYR);
RX MEDLINE-93304479; PubMed-8317544;
RA Wong D.T., Donoff R.B., Yang J., Song B.Z., Matossian K., Nagura N.,
RA Elovic A., McBride J., Gallagher G., Todd R.;
RT *Sequential expression of transforming growth factors alpha and beta 1
RT by eosinophils during cutaneous wound healing in the hamster.*;
RL Am. J. Pathol. 143:130-142(1993).
RN [2]
RP SEQUENCE OF 26-115 FROM N.A.
RC STRAIN-SYRIAN; TISSUE-SPLEEN;

DR SMART: SM00204; TGF β 1;
 DR PROSITE; PS00250; TGF_BETA_1: 1.
 FT NON_TER 124 124
 FT NON_TER 124 124
 SQ SEQUENCE 124 AA: 14329 MW: 21D185218E556DB CRC64;
 Query Match 31.2%; Score 674.5; DB 6; Length 124;
 Best Local Similarity 87.2%; Pred. No. 1.1e-51;
 Matches 123; Conservative 0; Mismatches 1; Indels 17; Gaps 1;
 QY 264 PLERAQHLSSRRRALDNTSYDVPDYASLADTNYCFSSSTKNCVCVQLYIDFRKDL 323
 Db 1 PLERAQHLSSRRRALDNTSYDVPDYASLADTNYCFSSSTKNCVCVQLYIDFRKDL 43
 QY 324 GWKWIHEPGYHANFCLGCPYIWSLDTOYSKVLALYNOHNPASAPCCVQALEPLPI 383
 Db 44 GWKWIHEPGYHANFCLGCPYIWSLDTOYSKVLALYNOHNPASAPCCVQALEPLPI 103
 QY 384 VYVVGKPKVEQLSNMIVRSC 404
 Db 104 VYVVGKPKVEQLSNMIVRSC 124
 RESULT 14
 Q98854 PRELIMINARY; PRT; 361 AA.
 AC Q98854;
 DT 01-FEB-1997 (TRENBLrel. 02, Created)
 DT 01-FEB-1997 (TRENBLrel. 02, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE Transforming growth factor beta 2 (TGF-beta 2) (fragment).
 GN TGF β 2.
 OS Cyprinus carpio (Common carp).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Cyprinus.
 OX NCBI_TaxID=7962;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=HEART;
 RX MEDLINE=97354301; PubMed=9210595;
 RA Sumathy K., Desai K.V., Kondiah P.;
 RT 'Isolation of transforming growth factor-beta2 cDNA from a fish,
 RT Cyprinus carpio by RT-PCR.';
 RL Gene 191:103-107(1997).
 CC -1- FUNCTION: TGF-BETA 2 HAS SUPPRESSIVE EFFECTS ON INTERLEUKIN-2
 CC DEPENDENT T-CELL GROWTH.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC EMBL; U66874; AAB62983.1; -.
 DR HSSP; P08112; 2TGI.
 DR InterPro; IPR001839; TGF β .
 DR InterPro; IPR001111; TGF β N.
 DR InterPro; IPR003911; TGF-TGF β .
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGF β -propeptide; 1.
 DR PRINTS; PR01423; TGF β BETA.
 DR ProDom; PD000357; TGF β 1.
 DR SMART; SM00204; TGF β 1.
 DR PROSITE; PS00250; TGF_BETA_1: 1.
 KW Growth factor; Mitogen; Glycoprotein.
 FT NON_TER 1 1
 FT PROPEP <1 257
 FT CHAIN 258 361
 FT DISULFID 264 273
 FT DISULFID 272 335
 FT DISULFID 334 334
 FT CARBOHYD 30 30
 FT CARBOHYD 98 98
 FT CARBOHYD 199 199
 FT NON_TER 361 361
 SQ SEQUENCE 361 AA: 41931 MW: 94D930FA970A3FD3 CRC64;

Query Match 31.2%; Score 673.5; DB 13; Length 361;
 Best Local Similarity 40.4%; Pred. No. 6.1e-51;
 Matches 155; Conservative 54; Mismatches 116; Indels 59; Gaps 14;
 QY 52 QILSKRLASPPSQGDVPPGP--LPEAVLALYNSTRDRVAGESVEPEPEPE-----ADYY 104
 Db 1 QILCKLKLSCPP--EIVPEEVSRIIAIYNSTRDLQEKANERAAATCERQRTGEYY 57
 QY 105 AKETRVLM---VFSNQIYDKFKGTHPSLMLNTSELREAVPEPVLRAELRLRL- 160
 Db 58 AKEVHKIDMQPFAENVPTKHY-NPYFRRLRFDVSSMEKNASN--LVKAELRIERLQ 113
 QY 161 --KLKV--BOHYELVQ-----KYSNDSRWYLSNRLAPSDSPWLSFDVTGVVROWLTRRE 212
 Db 114 NPKARVSEQRLELQILGHKDLTPTQRYIDSKVVVIRTEGEMLSFDVTAYSEWLHRD 173
 QY 213 AIEGFRLSAHSS-----DSKNTLHVEINGFNSG--RRGLATI----HGMNR 255
 Db 174 RNNGFKISLHCPCCTFVPSNNYIIPNKSEELANFAGIDDSFVHCGDLKMFKKRRHSQS 233
 QY 256 PFLLLMATPLERAQHLSSRRRALDNTSYDVPDYASLADTNYCFSSSTKNCVCVQL 315
 Db 234 PHLLEMLLPSYRLESQHKSHRQ-----KRALDAAFCFRNVQDNCLRLSL 277
 QY 316 YIDFKKDLCKWKIHEPGYHANFCLGCPYIWSLDTOYSKVLALYNOHNPASAPCCVP 375
 Db 278 YIDFKKDLCKWKIHEPGYHANFCLGCPYIWSLDTOYSKVLALYNOHNPASAPCCVP 337
 QY 376 QALEPLPIVYVGRKPKVEQLSNM 399
 Db 338 QDLEPLTILYVIGTKPKIEQLSNM 361
 RESULT 15
 O02730 PRELIMINARY; PRT; 112 AA.
 AC O02730; O97501;
 DT 01-JUL-1997 (TRENBLrel. 04, Created)
 DT 01-JUL-1997 (TRENBLrel. 04, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE Transforming growth factor beta 1 (TGF-beta 1) (fragment).
 GN TGF β 1 OR TGF-BETA-1.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Taylor T.K., James E.R., McGonigle S., Yoho E.R.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 2-99 FROM N.A.
 RA Inoue K., Kawabe Y., Kodama T.;
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: TGF-BETA 1 IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROLS
 CC PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
 CC TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF
 CC THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1
 CC REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND
 CC DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
 CC -1- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 CC EMBL; AF000133; AAB53806.1; -.
 DR EMBL; AB020217; BAA36950.1; -.
 DR HSSP; P01137; 1KLA.
 DR InterPro; IPR002400; GF_cysknot.
 DR InterPro; IPR001839; TGF β .
 DR Pfam; PF00019; TGF-beta; 1.
 DR PRINTS; PR00438; GFCYSKNOT.
 DR ProDom; PD000357; TGF β 1.
 DR SMART; SM00204; TGF β 1.
 DR PROSITE; PS00250; TGF_BETA_1: 1.
 KW Growth factor; Mitogen; Glycoprotein.

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FT NON_TER      1      1
FT CHAIN         1 112 TRANSFORMING GROWTH FACTOR BETA 1.
FT DISULFID      7 16  BY SIMILARITY.
FT DISULFID     15 78  BY SIMILARITY.
FT DISULFID     44 109 BY SIMILARITY.
FT DISULFID     48 111 BY SIMILARITY.
FT DISULFID     77 77  INTERCHAIN (BY SIMILARITY).
FT CONFLICT      2 3   LD -> FS (IN REF. 2).
FT CONFLICT     85 92  PLPIVYV -> ATAHRTTL (IN REF. 2).
SQ SEQUENCE    112 AA; 12795 MW; 53C5B7D46355A6F3 CRC64;

Query Match      29.6%; Score 638; DB 6; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.5e-48;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      296 ALDTNYCFSSTEKNCCVRQLYIDFRKDLGKWIHEPKGYHANFCLGPCPYIWSLDTQYSK 355
Db      1 ALDTNYCFSSTEKNCCVRQLYIDFRKDLGKWIHEPKGYHANFCLGPCPYIWSLDTQYSK 60

QY      356 VLALYNQHNPGASAPCCVPQALEPLPIVYVYGRKPKVEQLSNMIVRSCKS 407
Db      61 VLALYNQHNPGASAPCCVPQALEPLPIVYVYGRKPKVEQLSNMIVRSCKS 112
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Search completed: October 7, 2003, 18:04:16
Job time : 102 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:47:27 ; Search time 5308.15 Seconds
(without alignments)
10489.161 Million cell updates/sec

Title: US-10-017-372E-38
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
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2: gb_htg:*
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41:  em_htgo_other:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	1224.4	90.0	3206	4	PIGTGFB1A	M23703 Sus scrofa	
2	1208.6	88.8	1326	6	AX338213	AX338213 Sequence	
3	1205	88.5	1750	4	GGTGFB1	X12373 Porcine mRNA	
4	1134.8	83.4	1605	4	SSTGFB1	Y00111 Porcine mRNA	
5	1113.4	81.8	2221	4	AF461808	AF461808 Sus scrof	
6	993.8	73.0	1369	4	DOGTGFB1A	L34956 Canine tran	
7	982.8	72.2	2527	6	E00973	E00973 cDNA encodi	
8	982	72.2	2537	6	A06669	A06669 Synthetic m	
9	976	71.7	1173	4	OATGFB1	X76916 O.aries mRNA	
10	975.6	71.7	1780	9	BC000125	BC000125 Homo sapi	
11	975.6	71.7	1780	9	BC001180	BC001180 Homo sapi	
12	974.2	71.6	1561	9	AGMTGFB	M16658 Simian tran	
13	971.4	71.4	1821	6	E03028	E03028 DNA encodin	
14	971	71.3	1746	9	BC022242	BC022242 Homo sapi	
15	969.8	71.3	1560	6	I06216	I06216 Sequence 2	
16	969	71.2	2745	9	HSTGFB1	X02812 Human mRNA	
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18	950.4	69.8	1569	6	I06221	I06221 Sequence 3	
19	945.4	69.5	1561	6	I08275	I08275 Sequence 3	
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21	930.8	68.4	1173	12	BT007866	BT007866 Synthetic	
22	921.6	67.7	1173	4	ECRGFB1	X99438 E.caballus	
23	921.4	67.7	1176	6	AX615127	AX615127 Sequence	
24	919.8	67.6	1176	6	AX481432	AX481432 Sequence	
25	919.8	67.6	1176	6	AX615128	AX615128 Sequence	
26	915.2	67.2	1187	4	AF175709	AF175709 Equus cab	
27	892.4	65.6	1597	10	AF191297	AF191297 Cavia por	
28	864	63.5	1641	10	BC013738	BC013738 Mus muscu	
29	850.2	62.5	1579	10	MUSTGFRNA	M13177 Mouse trans	
30	850.2	62.5	2094	10	MMU009862	AJ009862 Mus muscu	
31	830.6	61.0	1585	10	RNTGFB1	X52498 Rat mRNA fo	
32	818.8	60.2	1117	4	BOVTGFB	M36271 Bovine tran	
33	794.2	58.4	1125	10	AF480858	AF480858 Sigmodon	

34	685.4	50.4	1675	6	I03310	I03310 Sequence 1
35	657.2	48.3	1376	6	AX528533	AX528533 Sequence
36	655.6	48.2	1389	6	AX528619	AX528619 Sequence
37	594.6	43.7	1352	6	AX528535	AX528535 Sequence
38	589.8	43.3	1350	6	AX528615	AX528615 Sequence
39	546.8	40.2	699	6	I05434	I05434 Sequence 4
40	357.6	26.3	650	6	AX336646	AX336646 Sequence
41	357.6	26.3	650	9	HUMTGFB1	M38449 Homo sapien
42	357.6	26.3	862	6	I03312	I03312 Sequence 3
43	354.4	26.0	489	6	AX455100	AX455100 Sequence
44	327.2	24.0	469	10	MATGFB1	X60296 M.auratus m
45	321.4	23.6	1256	5	CHKTGFB4	M31160 Gallus gall

ALIGNMENTS

RESULT 1

PIGTGFB1A

LOCUS PIGTGFB1A 3206 bp mRNA linear MAM 31-MAR-1995

DEFINITION Sus scrofa transforming growth factor beta-1 mRNA, complete cds.

ACCESSION M23703

VERSION M23703.1 GI:755044

KEYWORDS transforming growth factor-beta-1.

SOURCE Sus scrofa (pig)

ORGANISM Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1 (bases 1 to 3206)

AUTHORS Kondaiah,P., Van Obberghen-Schilling,E., Ludwig,R.L., Dhar,R., Sporn,M.B. and Roberts,A.B.

TITLE cDNA cloning of porcine transforming growth factor-beta 1 mRNAs. Evidence for alternate splicing and polyadenylation

JOURNAL J. Biol. Chem. 263 (34), 18313-18317 (1988)

MEDLINE 89054010

PUBMED 2461367

COMMENT On Apr 1, 1995 this sequence version replaced gi:341017.

Original source text: Sus scrofa (strain miniature swine) cDNA to mRNA.

FEATURES

source

Location/Qualifiers

1. .3206

/organism="Sus scrofa"

/mol_type="mRNA"

/strain="miniature swine"

/db_xref="taxon:9823"

/cell_type="peripheral blood lymphocyte"

gene

1. .3206

/gene="TGF-beta-1"

CDS

906. .2078

/gene="TGF-beta-1"

/codon_start=1

/product="transforming growth factor-beta-1"

/protein_id="AAA64616.1"

/db_xref="GI:755045"

/translation="MPPSGLRLLPLLLPLLWLLVLTTPGRPAAGLSTCKTIDMELVKRK
RIEAI RGQILSKLRLASPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEAD
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KLKVEQHVELYQKYSNDSWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAI EGFR
LSAHCSCDSKDN TLHVEINGFN SGRRGDLATI HGMNRPFLLLMATPLERAQHLHSSRH
RRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDT
QYSKVLALYNQHNP GASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS"
polyA_signal      3186.  .3191
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QY	6	CCGAGATGGCGCCTTCGGGGGCTGCGGGCTCTTGCCGCTGCTGCTGCCGCTGCTGTGGCTGC	65
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QY	66	TAGTGCTGACGCCTTGGCCGGCCGGCCGCCGACTGTCCACCTGCAAGACCATCGACATGG	125
Db	961	TAGTGCTGACGCCTTGGCCGGCCGGCCGCCGACTGTCCACCTGCAAGACCATCGACATGG	1020
QY	126	AGCTGGTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGC	185
Db	1021	AGCTGGTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGC	1080
QY	186	TTGCCAGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCGCTGCCTGAGGCAGTACTGG	245
Db	1081	TCGCCAGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCGCTGCCTGAGGCAGTACTGG	1140
QY	246	CTCTTTACAACAGTACCCGCGACCGGGTAGCCGGGGAAAAGTGTGAAACCGGAGCCCGAGC	305
Db	1141	CTCTTTACAACAGTACCCGCGACCGGGTAGCCGGGGAAAAGTGTGAAACCGGAGCCCGAGC	1200
QY	306	CAGAGGCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAGCGGCAACC	365
Db	1201	CAGAGGCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAGCGGCAACC	1260
QY	366	AAATCTATGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGG	425
Db	1261	AAATCTATGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGG	1320
QY	426	AGCTCCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGA	485
Db	1321	AGCTCCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGA	1380
QY	486	GGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCT	545
Db	1381	GGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCT	1440
QY	546	GGCGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGA CTACCGGAGTGGCTGTCCTTTG	605
Db	1441	GGCGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGA CTACCGGAGTGGCTGTCCTTTG	1500
QY	606	ATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCC	665

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Db      1561 TCAGTGCCCACTGTTCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGT 1620
Qy      726 TCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTACGGCATGAACCGGCCCTTCCTGC 785
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Db      1621 TCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTACGGCATGAACCGGCCCTTCCTGC 1680
Qy      786 TCCTCATGGCCACCCCGCTGGAGAGGGCCAGCACCTGCACAGCTCCCGGCACCGCCGAG 845
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Db      1681 TCCTCATGGCCACCCCGCTGGAGAGGGCCAGCACCTGCACAGCTCCCGGCACCGCCGA- 1739
Qy      846 CCCTGGATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCCTGGATA 905
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Db      1740 -----GCCCTGGATA 1749
Qy      906 CCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTCTACATTGACT 965
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Db      1750 CCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTCTACATTGACT 1809
Qy      966 TCCGGAAGGACCTGGGCTGGAAGTGGATTATGAACCCAAGGGCTACCATGCCAATTTCT 1025
      |||
Db      1810 TCCGGAAGGACCTGGGCTGGAAGTGGATTATGAACCCAAGGGCTACCATGCCAATTTCT 1869
Qy      1026 GCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTC 1085
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Db      1870 GCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTC 1929
Qy      1086 TGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCCGTGCTGCGTGCCGCAGGCGCTGG 1145
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Db      1930 TGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCCGTGCTGCGTGCCGCAGGCGCTGG 1989
Qy      1146 AGCCACTGCCCATCGTGTACTACGTGGGCGCAAGCCCAAGGTGGAGCAGCTGTCCAACA 1205
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Db      1990 AGCCACTGCCCATCGTGTACTACGTGGGCGCAAGCCCAAGGTGGAGCAGCTGTCCAACA 2049
Qy      1206 TGATCGTGCGTTCTGTCAAGTGCAGCTGAGGCCCCGCCCCGCCCACAGCCCCGCCACCC 1265
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Db      2050 TGATCGTGCGTTCTGTCAAGTGCAGCTGAGGCCCCGCCCCGCCCACAGCCCCGCCACCC 2109
Qy      1266 GGCAGGCCCGGCCCCACCCCCGCCCCGCTCACCGGGGCTGTATTTAAGGACATCGTGCCC 1325
      |||
Db      2110 GGCAGGCCCGGCCCCACCCCCGCCCCGCTCACCGGGGCTGTATTTAAGGACATCGTGCCC 2169
Qy      1326 CAAGCCCACTTGGGATCGATTAAAGCGGCCGCGA 1359
      |||
Db      2170 CAAGCCCACTTGGGATCGATTAAAGGTGGAGAGA 2203

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RESULT 2

AX338213

LOCUS AX338213 1326 bp DNA linear PAT 09-JAN-2002
 DEFINITION Sequence 1 from Patent WO0181404.
 ACCESSION AX338213
 VERSION AX338213.1 GI:18128750

KEYWORDS .

SOURCE Sus scrofa (pig)

ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1

AUTHORS Strober,W., Nakamura,K., Kitani,A. and Fuss,I.J.

TITLE Inducible plasmid vector encoding tgf_g(b) and uses thereof

JOURNAL Patent: WO 0181404-A 1 01-NOV-2001;
THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)

FEATURES Location/Qualifiers

source 1. .1326
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/mol_type="genomic DNA"
/db_xref="taxon:9823"

CDS 16. .1188
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD20538.1"
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/translation="MAPSGLRLLPLLLPLLLWLLVLTGPRPAAGLSTCKTIDMELVKRK
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LSAHSSSDSKDNTLHVEINGFNSGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRH
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BASE COUNT 263 a 438 c 392 g 233 t

ORIGIN

Query Match 88.8%; Score 1208.6; DB 6; Length 1326;
Best Local Similarity 95.4%; Pred. No. 2e-209;
Matches 1297; Conservative 0; Mismatches 9; Indels 53; Gaps 3;

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Qy	61	GCTGCTAGTGCTGACGCCTGGCCGGCCGGCCCGGACTGTCCACCTGCAAGACCATCGA	120
Db	66	GCTGCTAGTGCTGACGCCTGGCCGGCCGGCCCGGACTGTCCACCTGCAAGACCATCGA	125
Qy	121	CATGGAGCTGGTGAAGCGGAAGCGCATCGAGGCCATTTCGCGGCCAGATTCTGTCCAAGCT	180
Db	126	CATGGAGCTGGTGAAGCGGAAGCGCATCGAGGCCATTTCGCGGCCAGATTCTGTCCAAGCT	185
Qy	181	TCGGCTTGCCAGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGT	240
Db	186	TCGGCTCGCCAGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCCGT	245
Qy	241	ACTGGCTCTTTACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCC	300
Db	246	ACTGGCTCTTTACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCC	305
Qy	301	CGAGCCAGAGGCGGACTACTACGCCAAGGAGGTCAACCGCGTGCTAATGGTGGAAGCGG	360
Db	306	CGAGCCAGAGGCGGACTACTACGCCAAGGAGGTCAACCGCGTGCTAATGGTGGAAGCGG	365

Qy	361	CAACCAAATCTATGATAAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACAC	420
Db	366	CAACCAAATCTATGATAAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACAC	425
Qy	421	GTCGGAGCTCCGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCT	480
Db	426	GTCGGAGCTCCGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCT	485
Qy	481	GCTGAGGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGA	540
Db	486	GCTGAGGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGA	545
Qy	541	TTCCTGGCGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTACCGGAGTGGCTGTC	600
Db	546	TTCCTGGCGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTACCGGAGTGGCTGTC	605
Qy	601	CTTTGATGTACACCGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTT	660
Db	606	CTTTGATGTACACCGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTT	665
Qy	661	TCGCCTCAGTGCCCACTGTTCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAA	720
Db	666	TCGCCTCAGTGCCCACTCTTCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAA	725
Qy	721	CGGGTTCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTACGGCATGAACCGGCCCTT	780
Db	726	CGGGTTCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTACGGCATGAACCGGCCCTT	785
Qy	781	CCTGCTCCTCATGGCCACCCCGCTGGAGAGGGCCAGCACCTGCACAGCTCCCGGCACCG	840
Db	786	CCTGCTCCTCATGGCCACCCCGCTGGAGAGGGCCAGCACCTGCACAGCTCCCGGCACCG	845
Qy	841	CCGAGCCCTGGATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCCT	900
Db	846	CCGA-----GCCCCT	854
Qy	901	GGATACCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTCTACAT	960
Db	855	GGATACCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTCTACAT	914
Qy	961	TGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTATGAACCCAAGGGCTACCATGCCAA	1020
Db	915	TGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTATGAACCCAAGGGCTACCATGCCAA	974
Qy	1021	TTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCT	1080
Db	975	TTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCT	1034
Qy	1081	GGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCCGTGCTGCGTGCCGCAGGC	1140
Db	1035	GGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCCGTGCTGCGTGCCGCAGGC	1094
Qy	1141	GCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTC	1200
Db	1095	GCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTC	1154

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Qy      1201 CAACATGATCGTGCCTTCCTGCAAGTGCAGCTGAGGCCCCGCCCCGCCACAGCCCCGCC 1260
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Db      1155 CAACATGATCGTGCCTTCCTGCAAGTGCAGCTGA-GCCCCGCCCCGCCACAGCCCCGCC 1213

Qy      1261 CACCCGGCAGGCCCCGGCCCCACCCCCGCCCCGCTCACCGGGGCTGTATTTAAGGACATCG 1320
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Db      1214 CACCCGGCAGGCCCCGGCCCCACCCCCGCCCCGCTCACCGGGGCTGTATTTAAGGACATCG 1273

Qy      1321 TGCCCCAAGCCCACCTTGGGATCGATTAAAGCGGCCGCGA 1359
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Db      1274 TGCCCCAAGCCCAC-TGGGATCGATTAAAGGTGGAGAGA 1311

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RESULT 3

GGTGFB1

LOCUS GGTGFB1 1750 bp mRNA linear MAM 27-MAR-1996

DEFINITION Porcine mRNA for transforming growth factor-beta 1.

ACCESSION X12373

VERSION X12373.1 GI:63808

KEYWORDS transforming growth factor-beta 1.

SOURCE Sus scrofa (pig)

ORGANISM Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1 (bases 1 to 1750)

AUTHORS Jakowlew,S.B., Dillard,P.J., Sporn,M.B. and Roberts,A.B.

TITLE Nucleotide sequence of chicken transforming growth factor-beta 1
(TGF-beta 1)

JOURNAL Nucleic Acids Res. 16 (17), 8730 (1988)

MEDLINE 88335639

PUBMED 3166520

REFERENCE 2 (bases 1 to 1750)

AUTHORS Jakowlew,S.B.

TITLE Direct Submission

JOURNAL Submitted (14-JUL-1988) Jakowlew S.B., National Institute of
health, National Cancer Institute, Laboratory of Chemoprevention,
Building 41, Room B902, Bethesda, Maryland 20892, USA

COMMENT The submitters believe that the chicken cDNA library was
contaminated with porcine cDNA, and that the sequence is intact
porcine TGF-beta-1. 27-MAR-1996.

FEATURES Location/Qualifiers

source 1. .1750
/organism="Sus scrofa"
/mol_type="mRNA"
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gene 1. .1750
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5'UTR 1. .446
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CDS 447. .1622
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Qy	783	TGCTCCTCATGGCCACCCCGCTGGAGAGGGCCAGCACCTGCACAGCTCCCGGCACCGCC	842
Db	1222	TGCTCCTCATGGCCACCCCGCTGGAGAGGGCCAGCACCTGCACAGCTCCCGGCACCGCC	1281
Qy	843	GAGCCCTGGATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCCTGG	902
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Qy	963	ACTTCCGGAAGGACCTGGGCTGGAAGTGGATTATGAACCCAAGGGCTACCATGCCAATT	1022
Db	1351	ACTTCCGGAAGGACCTGGGCTGGAAGTGGATTATGAACCCAAGGGCTACCATGCCAATT	1410
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Qy	1083	CTCTGTACAACCAGCACAAACCGGGCGCGTCGGCGGGCGCGGTGCTGCGTGCCGCAGGCGC	1142
Db	1471	CTCTGTACAACCAGCACAAACCGGGCGCGTCGGCGGGCGCGGTGCTGCGTGCCGCAGGCGC	1530
Qy	1143	TGGAGCCACTGCCCATCGTGTAACGTGGGCGCGCAAGCCCAAGGTGGAGCAGCTGTCCA	1202
Db	1531	TGGAGCCACTGCCCATCGTGTAACGTGGGCGCGCAAGCCCAAGGTGGAGCAGCTGTCCA	1590
Qy	1203	ACATGATCGTGCGTTCTTGCAAGTGCAGCTGAGGCCCCGCCCCGCCACAGCCCCGCCCA	1262
Db	1591	ACATGATCGTGCGTTCTTGCAAGTGCAGCTGAGGCCCCGCCCCGCCACAGCCCCGCCCA	1650
Qy	1263	CCCGGCAGGCCCCGGCCCCACCCCCGCCCCCTACCGGGGCTGTATTTAAGGACATCGTG	1322
Db	1651	CCCGGCAGGCCCCGGCCCCACCCCCGCCCCCTACCGGGGCTGTATTTAAGGACATCGTG	1710
Qy	1323	CCCCAAGCCCACTTGGGATCGATTAAAGCGGCCGCGA	1359
Db	1711	CCCCAAGCCCACTTGGGATCGATTAAAGGTGGAGAGA	1747

SSTGFBR
 LOCUS SSTGFBR 1605 bp mRNA linear MAM 27-MAR-1995
 DEFINITION Porcine mRNA for transforming growth factor-beta (TFG) precursor.
 ACCESSION Y00111
 VERSION Y00111.1 GI:2129
 KEYWORDS transforming growth factor-beta.
 SOURCE Sus scrofa (pig)
 ORGANISM Sus scrofa
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 REFERENCE 1 (bases 1 to 1605)
 AUTHORS Derynck, R. and Rhee, L.
 TITLE Sequence of the porcine transforming growth factor-beta precursor
 JOURNAL Nucleic Acids Res. 15 (7), 3187 (1987)
 MEDLINE 87174844
 PUBMED 3470708
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 CDS 404..1576
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 ORIGIN

Query Match 83.4%; Score 1134.8; DB 4; Length 1605;
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 Matches 1200; Conservative 0; Mismatches 7; Indels 51; Gaps 1;

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 Db 399 CCCCCATGCCGCTTCGGGGCTGCGGCTCTTGCCGCTGCTGCTGCCGCTGCTGTGGCTGC 458
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 Db 459 TAGTGCTGACGCCTGGCCGGCCGGCCGGCCGACTGTCCACCTGCAAGACCATCGACATGG 518

QY	126	AGCTGGTGAAGCGGAAGCGCATCGAGGCCATTGCGGGCCAGATTCTGTCCAAGCTTCGGC	185
Db	519	AGCTGGTGAAGCGGAAGCGCATCGAGGCCATTGCGGGCCAGATTCTGTCCAAGCTTCGGC	578
QY	186	TTGCCAGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGG	245
Db	579	TCGCCAGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGG	638
QY	246	CTCTTTACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGC	305
Db	639	CTCTTTACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGC	698
QY	306	CAGAGGCGGACTACTACGCCAAGGAGGTACCCGCGTGCTAATGGTGGAAAGCGGCAACC	365
Db	699	CAGAGGCGGACTACTACGCCAAGGAGGTACCCGCGTGCTAATGGTGGAAAGCGGCAACC	758
QY	366	AAATCTATGATAAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGG	425
Db	759	AAATCTATGATAAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGG	818
QY	426	AGCTCCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGA	485
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QY	486	GGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCT	545
Db	879	GGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCT	938
QY	546	GGCGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGCGTGTCTTTG	605
Db	939	GGCGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGCGTGTCTTTG	998
QY	606	ATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCC	665
Db	999	ATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCC	1058
QY	666	TCAGTGCCCACTGTTCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGT	725
Db	1059	TCAGTGCCCACTGTTCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGT	1118
QY	726	TCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTACGGCATGAACCGGCCCTTCTGTC	785
Db	1119	TCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTACGGCATGAACCGGCCCTTCTGTC	1178
QY	786	TCCTCATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAG	845
Db	1179	TCCTCATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAG	1237
QY	846	CCCTGGATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCCTGGATA	905
Db	1238	-----GCCCTGGATA	1247
QY	906	CCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTCTACATTGACT	965
Db	1248	CCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTCTACATTGACT	1307
QY	966	TCCGGAAGGACCTGGGCTGGAAGTGGATTTCATGAACCCAAGGGCTACCATGCCAATTTCT	1025

Db	1308		TCCGGAAGGACCTGGGCTGGAAGTGGATTTCATGAACCCAAGGGCTACCATGCCAATTTCT	1367
Qy	1026		GCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTC	1085
Db	1368		GCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTC	1427
Qy	1086		TGTACAACCAGCACAAACCCGGGCGCGTCGGCGGCGCCGTGCTGCGTGCCGCAGGCGCTGG	1145
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Qy	1146		AGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACA	1205
Db	1488		AGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACA	1547
Qy	1206		TGATCGTGCGTTCCTGCAAGTGCAGCTGAGGCCCCGCCCCGCCACAGCCCCGCCAC	1263
Db	1548		TGATCGTGCGTTCCTGCAAGTGCAGCTGAGGCCCCGCCCCGCCACAGCCCCGCCAC	1605

RESULT 5

AF461808

LOCUS AF461808 2221 bp mRNA linear MAM 03-JAN-2002

DEFINITION Sus scrofa transforming growth factor beta 1 (TGFB1) mRNA, complete cds.

ACCESSION AF461808

VERSION AF461808.1 GI:18042250

KEYWORDS .

SOURCE Sus scrofa (pig)

ORGANISM Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE 1 (bases 1 to 2221)

AUTHORS Wimmers,K., Chomdej,S., Ponsuksili,S. and Schellander,K.

TITLE Polymorphism in the porcine transforming growth factor beta 1 gene

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 2221)

AUTHORS Wimmers,K., Chomdej,S., Ponsuksili,S. and Schellander,K.

TITLE Direct Submission

JOURNAL Submitted (20-DEC-2001) Institute of Animal Breeding Science, University of Bonn, Endenicher Allee 15, Bonn 53115, Germany

FEATURES Location/Qualifiers

source 1. .2221
/organism="Sus scrofa"
/mol_type="mRNA"
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gene 1. .2221
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CDS 1. .1173
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Db      661 GCCCACTGTTCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT 720
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Db      781 ATGGCCACCCCGCTGGAGAGGGCCAGCACCTGCACAGCTCCCGGCACCGCCGA----- 834
Qy      851 GATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCCTGGATACCAAC 910
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Db      850 TACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTCTACATTGACTTCCGG 909
Qy      971 AAGGACCTGGGCTGGAAGTGGATTTCATGAACCCAAGGGCTACCATGCCAATTTCTGCCTG 1030
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Db      910 AAGGACCTGGGCTGGAAGTGGATTTCATGAACCCAAGGGCTACCATGCCAATTTCTGCCTG 969
Qy      1031 GGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCTTGGCTCTGTAC 1090
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RESULT 6

DOGTGFB1A

LOCUS DOGTGFB1A 1369 bp mRNA linear MAM 30-OCT-1994

DEFINITION Canine transforming growth factor-beta 1 (TGFB1) mRNA, complete cds.

ACCESSION L34956

VERSION L34956.1 GI:516071

KEYWORDS homologue; transforming growth factor-beta 1.

SOURCE Canis familiaris (dog)

ORGANISM Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

REFERENCE 1 (bases 1 to 1369)

AUTHORS Manning,A.M., Auchampach,J.A., Drong,R.F. and Slightom,J.L.

Db	233	TCTCCAGCCCCCGAGCCAGGGGAGGTGCCCGCCGTGCCGCTGCCCGAGGCCGTGCTGG	292
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Db	293	CCCTCTACAACAGCACCCGCGACCGGGTGGCGGGGAGAGCGCCGAGCCCGAGCCCGAGC	352
Qy	306	CAGAGGCGGACTACTACGCCAAGGAGGTCAACCGCGTGCTAATGGTGGAAGCGGCAACC	365
Db	353	CCGAGGCGGACTACTACGCCAAGGAGGTCAACCGCGTGCTAATGGTGGAACACCAACA	412
Qy	366	AAATCTATGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGG	425
Db	413	AAATCTATGAGAAAGTCAAGAAAAGTCCGCACAGCATATATATGCTCTTCAACACATCAG	472
Qy	426	AGCTCCGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGA	485
Db	473	AGCTCCGAGAAGCAGTGCCTGAGCCCGTCTTGCTCTCCCGGGCAGAGTTGCGCCTGCTGA	532
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Qy	546	GGCGCTACCTCAGCAACCGGCTGCTGGCCCCAGTGACTCACCGGAGTGGCTGTCCTTTG	605
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Qy	606	ATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCC	665
Db	653	ATGTCACTGGAGTCGTGAGGCAGTGGCTGAGCCATGGAGGGGAAGTCGAGGGCTTTTCGCC	712
Qy	666	TCAGTGCCCACTGTTCCCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGT	725
Db	713	TCAGTGCCCACTGTTCCCTGTGACAGCAAAGATAACACACTGCAAGTAGACATTAACGGGT	772
Qy	726	TCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGC	785
Db	773	TCAGTTCAGCCGCCGAGGTGACCTGGCCACCATTCATGGCATGAACCGACCTTCCTGC	832
Qy	786	TCCTCATGGCCACCCCGCTGGAGAGGGCCAGCACCTGCACAGCTCCCGGCACCGCCGAG	845
Db	833	TCCTCATGGCCACCCACTGGAGAGGGCCAGCACCTGCACAGCTCCCGGCAGCGCCG--	890
Qy	846	CCCTGGATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCCTGGATA	905
Db	891	-----GGCCCTGGACA	901
Qy	906	CCAATACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTCTACATTGACT	965
Db	902	CCAATACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTCTACATTGACT	961
Qy	966	TCCGGAAGGACCTGGGCTGGAAGTGGATTTCATGAACCCAAGGGCTACCATGCCAATTTCT	1025
Db	962	TCCGCAAGGATCTGGGCTGGAAGTGGATCCATGAGCCCAAGGGTTACCACGCTAACTTCT	1021
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ORIGIN

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Query Match          72.2%;   Score 982.8;   DB 6;   Length 2527;
Best Local Similarity 85.1%;   Pred. No. 1.8e-168;
Matches 1144;   Conservative    0;   Mismatches 147;   Indels    53;   Gaps    2;

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Qy      6  CCGAGATGGCGCCTTCGGGGCTGCGGCTCTTGCCGCTGCTGCTGCCGCTGCTGTGGCTGC 65
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Db      837 CCCCCATGCCGCCCTCCGGGCTGCGGCTGCTGCCGCTGCTGCTACCGCTGCTGTGGCTAC 896

Qy      66 TAGTGCTGACGCCTGGCCGGCCGGCCCGGACTGTCCACCTGCAAGACCATCGACATGG 125
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Db      897 TGGTGCTGACGCCTGGCCCGCCGGCCCGGACTATCCACCTGCAAGACTATCGACATGG 956

Qy      126 AGCTGGTGAAGCGGAAGCGCATCGAGGCCATTCCGGGCCAGATTCTGTCCAAGCTTCGGC 185
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Db      957 AGCTGGTGAAGCGGAAGCGCATCGAGGCCATCCGGGCCAGATCCTGTCCAAGCTGCGGC 1016

Qy      186 TTGCCAGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCGCTGCCTGAGGCAGTACTGG 245
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Db      1017 TCGCCAGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCGCTGCCCAGGCCGTGCTCG 1076

Qy      246 CTCTTTACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGC 305
      | || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      1077 CCCTCTACAACAGCACCCGCGACCGGGTGGCCGGGGAGAGTGCAGAACCGGAGCCCGAGC 1136

Qy      306 CAGAGGCGGACTACTACGCCAAGGAGGTCAACCGCGTGCTAATGGTGGAAAGCGGCAACC 365
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Db      1137 CTGAGGCCGACTACTACGCCAAGGAGGTCAACCGCGTGCTAATGGTGGAAACCCACAACG 1196

Qy      366 AAATCTATGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGG 425
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Db      1197 AAATCTATGACAAGTTCAAGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAG 1256

Qy      426 AGCTCCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGA 485
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Qy      486 GGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCT 545
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Db      1317 GGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCT 1376

Qy      546 GGCGCTACCTCAGCAACCGGCTGCTGGCCCCAGTGACTACCGGAGTGGCTGTCTTTG 605
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LOCUS A06669 2537 bp mRNA linear PAT 29-JUL-1993
 DEFINITION Synthetic mRNA for preTGF-Beta1.
 ACCESSION A06669
 VERSION A06669.1 GI:412940
 KEYWORDS .
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.
 REFERENCE 1 (bases 1 to 2537)
 AUTHORS .
 TITLE NUCLEIC ACID ENCODING TGF- beta 3 AND ITS USE
 JOURNAL Patent: WO 8912101-A 4 14-DEC-1989;
 FEATURES Location/Qualifiers
 source 1..2537
 /organism="synthetic construct"
 /mol_type="mRNA"
 /db_xref="taxon:32630"
 CDS 842..2014
 /codon_start=1
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 /product="preTGF-beta1"
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 KLKVEQHVELYQKYSNNSWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFR
 LSAHCSCDSRDNTLQVDINGFTTGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRH
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 BASE COUNT 473 a 893 c 739 g 432 t
 ORIGIN

Query Match 72.2%; Score 982; DB 6; Length 2537;
 Best Local Similarity 84.9%; Pred. No. 2.5e-168;
 Matches 1148; Conservative 0; Mismatches 145; Indels 59; Gaps 2;

QY 6 CCGAGATGGCGCCTTCGGGGCTGCGGCTCTTGCCGCTGCTGCTGCCGCTGCTGTGGCTGC 65
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 Db 837 CCCCCATGCCGCCCTCCGGGCTGCGGCTGCTGCCGCTGCTGCTACCGCTGCTGTGGCTAC 896
 QY 66 TAGTGCTGACGCCTGGCCGGCCGGCCCGGACTGTCCACCTGCAAGACCATCGACATGG 125
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 Db 897 TGGTGCTGACGCCTGGCCCGCCGGCCCGGACTATCCACCTGCAAGACTATCGACATGG 956
 QY 126 AGCTGGTGAAGCGGAAGCGCATCGAGGCCATTCCGCGGCCAGATTCTGTCCAAGCTTCGGC 185
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 Db 957 AGCTGGTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGC 1016
 QY 186 TTGCCAGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCGCTGCCTGAGGCAGTACTGG 245
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 Db 1017 TCGCCAGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCGCTGCCCGAGGCCGTGCTCG 1076
 QY 246 CTCTTTACAACAGTACCCGCGACCGGGTAGCCGGGGGAAAGTGTCGAACCGGAGCCCGAGC 305
 ||| ||||||| ||||||| ||||||| ||||||| ||||| ||||||| |||||||
 Db 1077 CCCTGTACAACAGCACCCGCGACCGGGTGGCCGGGGGAGAGTGCAGAACCGGAGCCCGAGC 1136

Qy	306	CAGAGGCGGACTACTACGCCAAGGAGGTCAACCCGCGTGCTAATGGTGGAAGCGGCAACC	365
Db	1137	CTGAGGCCGACTACTACGCCAAGGAGGTCAACCCGCGTGCTAATGGTGGAAGCGGCAACC	1196
Qy	366	AAATCTATGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGG	425
Db	1197	AAATCTATGACAAGTTCAAGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAG	1256
Qy	426	AGCTCCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGA	485
Db	1257	AGCTCCGAGAAGCGGTACCTGAACCCGTGTGCTCTCCCGGGCAGAGCTGCGTCTGCTGA	1316
Qy	486	GGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCT	545
Db	1317	GGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCT	1376
Qy	546	GGCGCTACCTCAGCAACCGGCTGCTGGCCCCAGTGACTCACCGGAGTGGCTGTCCTTTG	605
Db	1377	GGCGATACCTCAGCAACCGGCTGCTGGCACCAGCGACTCGCCAGAGTGGTTATCTTTTG	1436
Qy	606	ATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGAGAGAGGCTATAGAGGGTTTTCGCC	665
Db	1437	ATGTCACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTTCGCC	1496
Qy	666	TCAGTGCCCACTGTTCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGT	725
Db	1497	TTAGCGCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGAATCAACGGGT	1556
Qy	726	TCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTACCGGCATGAACCGGCCCTTCTGTC	785
Db	1557	TCACTACCGGCCGCCGAGGTGACCTGGCCACCATTATGGCATGAACCGGCCCTTCTGTC	1616
Qy	786	TCCTCATGGCCACCCCGCTGGAGAGGGCCAGCACCTGCACAGCTCCCGGCACCGCCGAG	845
Db	1617	TTCTCATGGCCACCCCGCTGGAGAGGGCCAGCATCTGCAAAGCTCCCGGCACCGCCGA-	1675
Qy	846	CCCTGGATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCCTGGATA	905
Db	1676	-----GCCCTGGACA	1685
Qy	906	CCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTCTACATTGACT	965
Db	1686	CCAACTATTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTGTACATTGACT	1745
Qy	966	TCCGGAAGGACCTGGGCTGGAAGTGGATTATGAACCCAAGGGCTACCATGCCAATTTCT	1025
Db	1746	TCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCATGCCAATTTCT	1805
Qy	1026	GCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTC	1085
Db	1806	GCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAGGTCCTGGCCC	1865
Qy	1086	TGTACAACCAGCACAACCCGGGCGCGTCCGGCGCGCCGTGCTGCGTGCCGCAGGCGCTGG	1145
Db	1866	TGTACAACCAGCATAACCCGGGCGCCTCGGCGGCGCCGTGCTGCGTGCCGCAGGCGCTGG	1925
Qy	1146	AGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACA	1205

Db	1926	AGCCGCTGCCCATCGTGTA	CTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACA	1985
Qy	1206	TGATCGTGCGTTTCCTGCAAGTGCAGCTGAGGCCCCGCCCCGCCACAGCCCCGCCACCC		1265
Db	1986	TGATCGTGCGCTCCTGCAAGTGCAGCTGAGGTCCC	GCCCCGCCCGCCCCGCCCGCCCGGCAG	2045
Qy	1266	GGCAGGCCCGGCCCCACCCCCGCCGCCT-----CACCGGGGCTGTATT	TAAAGGACA	1317
Db	2046	GCCCGGCCCCACCCCCGCCCGCCCCGCTGCCTTGCCCATGGGGGCTGTATT	TAAAGGACA	2105
Qy	1318	TCGTGCCCCAAGCCCACTTGGGATCGATTAA		1349
Db	2106	CCGTGCCCCAAGCCCACTGGGGGCCCATTA		2137

RESULT 9

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OATGFB1
LOCUS      OATGFB1              1173 bp      mRNA      linear      MAM 18-APR-1995
DEFINITION O.aries mRNA for transforming growth factor-beta I.
ACCESSION  X76916
VERSION    X76916.1   GI:496648
KEYWORDS   TGF-beta 1; transforming growth factor-beta 1.
SOURCE     Ovis aries (sheep)
  ORGANISM Ovis aries
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Caprinae; Ovis.
REFERENCE  1
  AUTHORS  Woodall,C.J., McLaren,L.J. and Watt,N.J.
  TITLE    Sequence and chromosomal localisation of the gene encoding ovine
            latent transforming growth factor-beta 1
  JOURNAL  Gene 150 (2), 371-373 (1994)
  MEDLINE  95121932
  PUBMED   7821809
REFERENCE  2 (bases 1 to 1173)
  AUTHORS  Woodall,C.
  TITLE    Direct Submission
  JOURNAL  Submitted (24-DEC-1993) C. Woodall, Univ. of Edinburgh, Dept. of
            Veterinary Pathology, Sc. of Vet. Studies, Univ. of Edinburgh,
            Edinburgh EH9 1QH, UK
FEATURES   Location/Qualifiers
    source  1. .1173
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            /db_xref="taxon:9940"
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            /protein_id="CAA54242.1"
            /db_xref="GI:496649"
            /db_xref="SWISS-PROT:P50414"
            /translation="MPPSGLRLLPLLLPLLLWLLMLTTPGRPVAGLSTCKTIDMELVKRK
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Db      661 GCCCACTGTTCTGTGACAGTAAGGATAACACGCTTCAAGTGGACATCAACGGGTTTCAGT 720
Qy      731 TCTGGCCGCCGGGGTGACCTGGCCACCATTACGGCATGAACCGGCCCTTCCTGCTCCTC 790
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Db      721 TCCGGCCGCCGGGGTGACCTCGCCACCATTACGGCATGAACCGGCCCTTCCTGCTCCTC 780
Qy      791 ATGGCCACCCCGCTGGAGAGGGCCAGCACCTGCACAGCTCCCGGCACCGCCGAGCCCTG 850
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Db      781 ATGGCCACCCCTCTGGAGAGGGCCAGCACCTGCACAGCTCCCGCCACCGCCGA----- 834
Qy      851 GATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCCTGGATACCAAC 910
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Db      835 -----GCCCTGGACACCAAC 849
Qy      911 TACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTCTACATTGACTTCCGG 970
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Db      850 TACTGCTTCAGCTCCACAGAAAAGAACTGCTGTGTTTCGTCAGCTCTACATTGACTTCCGG 909
Qy      971 AAGGACCTGGGCTGGAAGTGGATTTCATGAACCCAAGGGCTACCATGCCAATTTCTGCCTG 1030
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Db      910 AAGGACCTGGGCTGGAAGTGGATTTCACGAACCCAAGGGCTACCACGCCAATTTCTGCCTG 969
Qy      1031 GGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTCTGTAC 1090
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Db      970 GGGCCCTGTCCCTACATCTGGAGCCTGGACACACAGTACAGCAAGGTCCTGGCCCTGTAC 1029
Qy      1091 AACCAGCACAACCCGGGCGCGTCCGGCGGCCCGTGCTGCGTGCCGCAGGCGCTGGAGCCA 1150
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Db      1030 AACCAGCACAACCCGGGCGCATCCGGCGGCCCGTGCTGCGTGCCCTCAGGCGCTGGAACCC 1089
Qy      1151 CTGCCCATCGTGTACTACGTGGGCGCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATC 1210
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Db      1090 CTGCCCATCGTGTACTACGTGGGCGCGCAAGCCCAAGGTGGAGCAGTTGTCCAACATGATC 1149
Qy      1211 GTGCGTTCCTGCAAGTGCAGCTGA 1234
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Db      1150 GTGCGCTCCTGCAAGTGCAGCTGA 1173

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RESULT 10

BC000125

LOCUS BC000125 1780 bp mRNA linear PRI 12-JUL-2001

DEFINITION Homo sapiens, Similar to transforming growth factor, beta 1, clone MGC:3119 IMAGE:3351664, mRNA, complete cds.

ACCESSION BC000125

VERSION BC000125.1 GI:12652748

KEYWORDS MGC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1780)

AUTHORS Strausberg,R.

TITLE Direct Submission

JOURNAL Submitted (03-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

Qy	66	TAGTGCTGACGCCTGGCCGGCCGGCCGCCGGACTGTCCACCTGCAAGACCATCGACATGG	125
Db	502	TGGTGCTGACGCCTGGCCGGCCGGCCGCCGGGACTATCCACCTGCAAGACTATCGACATGG	561
Qy	126	AGCTGGTGAAGCGGAAGCGCATCGAGGCCATTTCGCGGCCAGATTCTGTCCAAGCTTCGGC	185
Db	562	AGCTGGTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGC	621
Qy	186	TTGCCAGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCGCTGCCTGAGGCAGTACTGG	245
Db	622	TCGCCAGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCGCTGCCCCGAGGCCGTGCTCG	681
Qy	246	CTCTTTACAACAGTACCCGCGACCGGGTAGCCGGGGAAAAGTGTGAAACCGGAGCCCGAGC	305
Db	682	CCCTGTACAACAGCACCCGCGACCGGGTGGCCGGGGAGAGTGCAGAAACCGGAGCCCGAGC	741
Qy	306	CAGAGGCGGACTACTACGCCAAGGAGGTCAACCGCTGCTAATGGTGAAAGCGGCAACC	365
Db	742	CTGAGGCCGACTACTACGCCAAGGAGGTCAACCGCTGCTAATGGTGAAACCCACAACG	801
Qy	366	AAATCTATGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGG	425
Db	802	AAATCTATGACAAGTTCAAGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAG	861
Qy	426	AGCTCCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGA	485
Db	862	AGCTCCGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGCAGAGCTGCGTCTGCTGA	921
Qy	486	GGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCT	545
Db	922	GGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCT	981
Qy	546	GGCGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGA CTACCGGAGTGGCTGTCCTTTG	605
Db	982	GGCGATACTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTG	1041
Qy	606	ATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGAGAGAGGCTATAGAGGGTTTTCGCC	665
Db	1042	ATGTCACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTTCGCC	1101
Qy	666	TCAGTGCCCACTGTTCTGTGACAGCAAAGATAACACACTCCAGTGGAATTAACGGGT	725
Db	1102	TTAGCGCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGACATCAACGGGT	1161
Qy	726	TCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTACGGCATGAACCGGCCCTTCCTGC	785
Db	1162	TCACTACCGGCCGCCGAGGTGACCTGGCCACCATTATGGCATGAACCGGCCCTTCCTGC	1221
Qy	786	TCCTCATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAG	845
Db	1222	TTCTCATGGCCACCCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGCCGA-	1280
Qy	846	CCCTGGATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCCTGGATA	905
Db	1281	-----GCCCTGGACA	1299

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RESULT 11
BC001180
LOCUS          BC001180              1780 bp      mRNA      linear      PRI 12-JUL-2001
DEFINITION     Homo sapiens, Similar to transforming growth factor, beta 1, clone
                MGC:2323 IMAGE:3356605, mRNA, complete cds.
ACCESSION      BC001180
VERSION        BC001180.1  GI:12654682
KEYWORDS       MGC.
SOURCE         Homo sapiens (human)
                ORGANISM  Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1  (bases 1 to 1780)
AUTHORS        Strausberg,R.
TITLE          Direct Submission
JOURNAL        Submitted (11-DEC-2000) National Institutes of Health, Mammalian
                Gene Collection (MGC), Cancer Genomics Office, National Cancer
                Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                USA
REMARK         NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT        Contact: MGC help desk
                Email: cgapbs-r@mail.nih.gov
                Tissue Procurement: ATCC
                cDNA Library Preparation: Rubin Laboratory

```

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Genome Sequence Centre,
 BC Cancer Agency, Vancouver, BC, Canada
 info@bcgsc.bc.ca
 Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
 Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
 Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
 Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
 Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline
 Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott,
 Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
 George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAL Plate: 6 Row: e Column: 10
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 37097.

FEATURES	Location/Qualifiers
source	1. .1780 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="MGC:2323 IMAGE:3356605" /tissue_type="Eye, retinoblastoma" /clone_lib="NIH MGC_16" /lab_host="DH10B-R" /note="Vector: pOTB7"
CDS	447. .1619 /codon_start=1 /product="Similar to transforming growth factor, beta 1" /protein_id="AAH01180.1" /db_xref="GI:12654683" /translation="MPPSGLRLLLLLLPLLLWLLVLTGPRPAAGLSTCKTIDMELVKRK RIEAIRGQILSKRLASPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEAD YYAKEVTRVLMVETHNEIYDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRL KLVKVEQHVELYQKYSNNSWRYLNSRLLAPSDSPEWLSFDVTGVVRQWLRSRGGEIEGFR LSAHCSDSRDNTLQVDINGFTTGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRH RRALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDT QYSKVLALYNQHNPGASAAPCCVPQALEPLIVYYVGRKPKVEQLSNMIVRSCKCS"
BASE COUNT	341 a 648 c 493 g 298 t
ORIGIN	

Query Match 71.7%; Score 975.6; DB 9; Length 1780;
 Best Local Similarity 84.6%; Pred. No. 3.7e-167;
 Matches 1144; Conservative 0; Mismatches 149; Indels 59; Gaps 2;

Qy	6	CCGAGATGGCGCCTTCGGGGCTGCGGCTCTTGCCGCTGCTGCTGCCGCTGCTGTGGCTGC	65
Db	442	CCCCCATGCCGCCCTCCGGGCTGCGGCTGCTGCTGCTGCTACCGCTGCTGTGGCTAC	501
Qy	66	TAGTGCTGACGCCTGGCCGGCCGGCCGGCCGACTGTCCACCTGCAAGACCATCGACATGG	125
Db	502	TGGTGCTGACGCCTGGCCGGCCGGCCGGCCGACTATCCACCTGCAAGACTATCGACATGG	561
Qy	126	AGCTGGTGAAGCGGAAGCGCATCGAGGCCATTGCGGGCCAGATTCTGTCCAAGCTTCGGC	185

Db	562	AGCTGGTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGC	621
Qy	186	TTGCCAGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGG	245
Db	622	TCGCCAGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGCTGCCCGAGGCCGTGCTCG	681
Qy	246	CTCTTTACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTGAAACCGGAGCCCGAGC	305
Db	682	CCCTGTACAACAGCACCCGCGACCGGGTGGCCGGGGAGAGTGCAGAAACCGGAGCCCGAGC	741
Qy	306	CAGAGGCGGACTACTACGCCAAGGAGGTCAACCGCGTGCTAATGGTGGAAAGCGGCAACC	365
Db	742	CTGAGGCCGACTACTACGCCAAGGAGGTCAACCGCGTGCTAATGGTGGAAACCCACAACG	801
Qy	366	AAATCTATGATAAAATTCAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGG	425
Db	802	AAATCTATGACAAGTTCAGGAGAGTACACACAGCATATATATGTTCTTCAACACATCAG	861
Qy	426	AGCTCCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGA	485
Db	862	AGCTCCGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGCAGAGCTGCGTCTGCTGA	921
Qy	486	GGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCTT	545
Db	922	GGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCTT	981
Qy	546	GGCGCTACCTCAGCAACCGGCTGCTGGCCCCAGTGACTACCGGAGTGGCTGTCCTTTG	605
Db	982	GGCGATACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGTTATCTTTTG	1041
Qy	606	ATGTCAACGGAGTTGTGCGGCAGTGGCTGACCCGAGAGAGGCTATAGAGGGTTTTTCGCC	665
Db	1042	ATGTCAACGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTTCGCC	1101
Qy	666	TCAGTGCCCACTGTTTCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGT	725
Db	1102	TTAGCGCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGT	1161
Qy	726	TCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTACGGCATGAACCGGCCCTTCTGTC	785
Db	1162	TCACTACCGGCCGCCGAGGTGACCTGGCCACCATTATGGCATGAACCGGCCTTCTGTC	1221
Qy	786	TCCTCATGGCCACCCCGCTGGAGAGGGCCAGCACCTGCACAGCTCCCGGCACCGCCGAG	845
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Qy	846	CCCTGGATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCCTGGATA	905
Db	1281	-----GCCCTGGACA	1290
Qy	906	CCAATACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTCTACATTGACT	965
Db	1291	CCAATAATTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTGTACATTGACT	1350
Qy	966	TCCGGAAGGACCTGGGCTGGAAGTGGATTTCATGAACCAAGGGCTACCATGCCAATTTCT	1025
Db	1351	TCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCATGCCAATTTCT	1411

Qy	1026	GCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTC	1085
Db	1411	GCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAGGTCCTGGCCC	1470
Qy	1086	TGTACAACCAGCACAAACCGGGCGCGTCGGCGGCGCCGTGCTGCGTGCCGCAGGCGCTGG	1145
Db	1471	TGTACAACCAGCATAAACCGGGCGCCTCGGCGGCGCCGTGCTGCGTGCCGCAGGCGCTGG	1530
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Db	1531	AGCCGCTGCCCATCGTGTA CTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACA	1590
Qy	1206	TGATCGTGCGTTCCTGCAAGTGCAGCTGAGGCCCGCCCCGCCACAGCCCCGCCACCC	1265
Db	1591	TGATCGTGCGCTCCTGCAAGTGCAGCTGAGGTCCCGCCCCGCCCGCCCCGCCCGGCGAG	1650
Qy	1266	GGCAGGCCCGGCCCCACCCCCGCCCGCT-----CACCGGGGCTGTATTTAAGGACA	1317
Db	1651	GCCCCGCCCCACCCCCGCCCGCCCCGCTGCCTTGCCCATGGGGGCTGTATTTAAGGACA	1710
Qy	1318	TCGTGCCCCAAGCCCACTTGGGATCGATTAA	1349
Db	1711	CCCGTGCCCCAAGCCCACTTGGGGCCCCATTAA	1742

AGMTGFB

DEFINITION Simian transforming growth factor-beta (TGF) mRNA, complete cds.

ACCESSION M16658

KEYWORDS growth factor; tran

ORGANISM Cercopithecus aethiops

REFERENCE 1 (bases 1 to 1561)

TITLE	Cloning and sequence analysis of simian transforming growth factor-beta cDNA
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JOURNAL DNA 6 (3), 239-244 (1987)

PUBMED 3474130

FEATURES	Location/Qualifiers
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Best Local Similarity 85.0%;  Pred. No. 6.8e-167;
Matches 1150;  Conservative 0;  Mismatches 143;  Indels 60;  Gaps 3;

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Db      317 TGGTGCTGACGCCTAGCCGGCCGGCCGGCAGGACTATCCACCTGCAAGACTATCGACATGG 376

Qy      126 AGCTGGTGAAGCGGAAGCGCATCGAGGCCATTCCGGGCCAGATTCTGTCCAAGCTTCGGC 185
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Db      377 AGCTGGTGAAGCGGAAGCGCATCGAGACCATCCGGGCCAGATCCTGTCCAAGCTGCGGC 436

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Qy      246 CTCTTTACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGC 305
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Qy      306 CAGAGGCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAGCGGCAACC 365
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Db      557 CGGAGGCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAACCCACAACG 616

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Qy      426 AGCTCCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGA 485
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Qy	66	TAGTGCTGACGCCTGGCCGCGCCGCGGACTGTCCACCTGCAAGACCATCGACATGG	125
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Qy	126	AGCTGGTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGC	185
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Qy	186	TTGCCAGCCCCCGAGCCAGGGGGACGTGCCGCCCGCCGCTGCCTGAGGCAGTACTGG	245
Db	687	TCGCCAGCCCCCGAGCCAGGGGGAGGTGCCGCCCGCCGCTGCCCGAGGCCGTGCTCG	746
Qy	246	CTCTTTACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTGCAACCGGAGCCCGAGC	305
Db	747	CCCTGTACAACAGCACCCGCGACCGGGTGGCCGGGGAGAGTGCAGAACCGGAGCCCGAGC	806
Qy	306	CAGAGGCGGACTACTACGCCAAGGAGGTCAACCCGCGTGCTAATGGTGGAAAGCGGCAACC	365
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Qy	366	AAATCTATGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGG	425
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Qy	426	AGCTCCGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGA	485
Db	927	AGCTCCGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGA	986
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Qy	546	GGCGCTACCTCAGCAACCGGCTGCTGGCCCCAGTGACTCACCGGAGTGGCTGTCCTTTG	605
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Db	1107	ATGTCACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTTCGCC	1166
Qy	666	TCAGTGCCCACTGTTCCCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTACGGGT	725
Db	1167	TTAGCGCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGT	1226
Qy	726	TCAATTCTGGCCGCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGC	785
Db	1227	TCATAACCGGCCGCGGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCTTCCTGC	1286
Qy	786	TCCTCATGGCCACCCGCTGGAGAGGGCCAGCACCTGCACAGCTCCCGGCACCGCCGAG	845
Db	1287	TTCTCATGGCCACCCGCTGGAGAGGGCCAGCATCTGCAAAGCTCCCGGCACCGCCGA-	1345
Qy	846	CCCTGGATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCCTGGATA	905
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[illegible]

cdNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 27 Row: e Column: 21
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

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Best Local Similarity 84.8%; Pred. No. 2.5e-166;
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Qy      66 TAGTGCTGACGCCTGGCCGGCCGGCCGCGGACTGTCCACCTGCAAGACCATCGACATGG 125
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Qy	786	TCCTCATGGCCACCCCGCTGGAGAGGGCCAGCACCTGCACAGCTCCCGGCACCGCCGAG	845
Db	1145	TTCTCATGGCCACCCCGCTGGAGAGGGCCAGCATCTGCAAAGCTCCCGGCACCGCCGA-	1203
Qy	846	CCCTGGATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCCTGGATA	905
Db	1204	-----GCCCTGGACA	1213
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VERSION        I06216.1  GI:590649
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   ORGANISM    Unknown.
               Unclassified.
REFERENCE      1  (bases 1 to 1560)
   AUTHORS     Purchio,A.F., Gentry,L. and Twardzik,D.
   TITLE       Cloning and expression of simian transforming growth factor-SS1
   JOURNAL      Patent: EP 0293785-A2 2 07-DEC-1988;
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Db		321 CTGACGCCTAGCCGGCCGGCCGAGGACTATCCACCTGCAAGACTATCGACATCGAGCTG	380
Qy		131 GTGAAGCGGAAGCGCATCGAGGCCATTGCGGGCCAGATTCTGTCCAAGCTTCGGCTTGCC	190
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Qy 191 AGCCCCCGAGCCAGGGGGACGTGCCGCCCCGGCCCCGCTGCCTGAGGCAGTACTGGCTCTT 250
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		Query	Match Length			
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2	982.8	72.2	2527	25	ABQ76674	Androgen receptor
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4	982	72.2	2537	11	AAQ03301	cDNA encoding huma
5	982	72.2	2537	11	AAQ02814	Sequence of pre-TG
6	982	72.2	2537	17	AAT15720	Pre-transforming g
7	980.4	72.0	2537	15	AAQ56923	Human pre-TGF-beta
8	977.2	71.8	2537	19	AAV52933	Human pre-transfor
9	974.2	71.6	1561	11	AAQ03268	Simian transformin
10	972.6	71.5	2742	22	AAI58342	Human polynucleoti
11	971.8	71.4	1559	13	AAQ20289	Sequence encoding
12	971.4	71.4	1821	12	AAQ13392	Human pro-TGF-beta
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16	969	71.2	2745	22	AAH28216	Nucleotide sequenc
17	961	70.6	1303	11	AAQ09317	Monkey transformin
18	960	70.5	4105	15	AAQ55624	TGFbeta1 5'-UTR-CD
19	958	70.4	1571	11	AAQ03269	Human transforming
20	953	70.0	1569	9	AAN81085	Coding sequence of
21	949.8	69.8	1569	11	AAQ03509	Human Transforming
22	943.8	69.3	1561	11	AAQ04908	Sequence encoding
23	940.6	69.1	1561	13	AAQ29177	TGF-beta 1/beta 2

	24	921.4	67.7	1176	25	ABV75391	TGFB1 Arg25Pro pol
	25	919.8	67.6	1176	24	ABZ35738	Human TGF beta 1 p
	26	919.8	67.6	1176	24	ABX09981	Human TGFbeta1 DNA
	27	919.8	67.6	1176	24	ABV78162	Human TGF beta 1 D
	28	919.8	67.6	1176	24	ABL91703	Human polynucleoti
	29	919.8	67.6	1176	25	ABV75392	TGFB1 Arg25Pro pol
	30	899.2	66.1	1565	13	AAQ29178	TGF-beta 1. Homo
c	31	800.6	58.8	2765	22	AAI60128	Human polynucleoti
	32	779.4	57.3	2208	13	AAQ20291	Sequence encoding
	33	777.8	57.1	2206	11	AAQ03510	Human Transforming
	34	777.8	57.1	2207	11	AAQ03511	Hybrid transformin
	35	776.2	57.0	2207	11	AAQ05127	Human TGF-Beta1/TG
	36	764.8	56.2	2217	10	AAN90768	Sequence of human
	37	758.6	55.7	2200	16	AAT04115	Simian-human hybri
c	38	687.8	50.5	2773	23	AAS84421	DNA encoding novel
	39	682	50.1	834	12	AAQ12192	Sequence encoding
	40	657.2	48.3	1376	24	ABK90341	DNA encoding LAP-m
	41	655.6	48.2	1389	24	ABK90344	DNA encoding LAP-h
	42	591.4	43.5	1352	24	ABK90342	DNA encoding mIFNB
	43	589.8	43.3	1350	24	ABK90343	DNA encoding huIFN
	44	525.8	38.6	875	23	AAS70979	DNA encoding novel
	45	357.6	26.3	650	24	ABK84023	Human cDNA differe

ALIGNMENTS

RESULT 1

AAD22696

ID AAD22696 standard; cDNA; 1326 BP.

XX

AC AAD22696;

XX

DT 26-FEB-2002 (first entry)

XX

DE Porcine transforming growth factor beta 1 (TGF-beta1) cDNA.

XX

KW Porcine; transforming growth factor beta 1; TGF-beta1; gene therapy;

KW IBD; inflammatory bowel disease; autoimmune disease; immunosuppressive;

KW multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;

KW diabetes mellitus; sarcoidosis; psoriasis; dermatological; ss.

XX

OS Sus scrofa.

XX

FH Key Location/Qualifiers

FT CDS 16..1188

FT /*tag= a

FT /product= "Porcine TGF-beta1 mutant protein"

XX

PN WO200181404-A2.

XX

PD 01-NOV-2001.

XX

PF 20-APR-2001; 2001WO-US12980.

XX

PR 20-APR-2000; 2000US-199014P.

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Strober W, Nakamura K, Kitani A, Fuss IJ;

XX

DR WPI; 2002-026155/03.

DR P-PSDB; AAE13596.

XX

PT Composition for treating autoimmune diseases e.g. inflammatory bowel
PT disease in humans, comprises vector containing transforming growth
PT factor-beta under the control of inducible promoter -

XX

PS Claim 1; Fig 1; 78pp; English.

XX

CC The invention relates to a composition containing a vector comprising a
CC gene encoding a regulatory transcription factor under the control of a
CC promoter encoding a transforming growth factor-beta (TGF-beta). The
CC vector is useful for expressing TGF-beta, such as TGF-beta1, TGF-beta2
CC or TGF-beta3, its variants or homologues, by transfecting a cell which
CC is part of a host suspected of having an autoimmune disease, especially
CC inflammatory bowel disease (IBD), under conditions such that the
CC polypeptide encoded by the nucleic acid sequence in the vector is
CC expressed. The vector is delivered using a delivery system. The delivery
CC of the vector results in substantial elimination of symptoms of the
CC autoimmune disease and increased production of IL-10 by the host. The
CC composition is useful for treating various diseases with an autoimmune
CC component such as multiple sclerosis, rheumatoid arthritis, systemic
CC lupus erythematosus, insulin-dependent diabetes mellitus, sarcoidosis
CC and psoriasis, and also for assaying the expression of a gene in a cell.
CC The vector is further useful for screening of the effect of test
CC compounds on cytokine (e.g. TGF-beta) expression of transfected cells.
CC The present sequence is a cDNA encoding porcine TGF-beta1 mutant.

XX

SQ Sequence 1326 BP; 263 A; 438 C; 392 G; 233 T; 0 other;

Query Match 88.8%; Score 1208.6; DB 24; Length 1326;
Best Local Similarity 95.4%; Pred. No. 4.4e-235;
Matches 1297; Conservative 0; Mismatches 9; Indels 53; Gaps 3;

Qy	1	TGGTACCGAGATGGCGCCTTCGGGGCTGCGGCTCTTGCCGCTGCTGCTGCCGCTGCTGTG	60
Db	6	TGGTACCGAGATGGCGCCTTCGGGGCTGCGGCTCTTGCCGCTGCTGCTGCCGCTGCTGTG	65
Qy	61	GCTGCTAGTGCTGACGCCTGGCCGGCCGGCCCGGACTGTCCACCTGCAAGACCATCGA	120
Db	66	GCTGCTAGTGCTGACGCCTGGCCGGCCGGCCCGGACTGTCCACCTGCAAGACCATCGA	125
Qy	121	CATGGAGCTGGTGAAGCGGAAGCGCATCGAGGCCATTTCGCGGCCAGATTCTGTCCAAGCT	180
Db	126	CATGGAGCTGGTGAAGCGGAAGCGCATCGAGGCCATTTCGCGGCCAGATTCTGTCCAAGCT	185
Qy	181	TCGGCTTGCCAGCCCCCGAGCCAGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGT	240
Db	186	TCGGCTCGCCAGCCCCCGAGCCAGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCCGT	245
Qy	241	ACTGGCTCTTTACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCC	300
Db	246	ACTGGCTCTTTACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCC	305

Qy	301	CGAGCCAGAGGCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGAAAAGCGG	360
Db	306	CGAGCCAGAGGCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGAAAAGCGG	365
Qy	361	CAACCAAATCTATGATAAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACAC	420
Db	366	CAACCAAATCTATGATAAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACAC	425
Qy	421	GTCGGAGCTCCGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCT	480
Db	426	GTCGGAGCTCCGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCT	485
Qy	481	GCTGAGGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTATAACCAGAAAATACAGCAATGA	540
Db	486	GCTGAGGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTATAACCAGAAAATACAGCAATGA	545
Qy	541	TTCCTGGCGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTACCCGAGTGGCTGTC	600
Db	546	TTCCTGGCGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTACCCGAGTGGCTGTC	605
Qy	601	CTTTGATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTT	660
Db	606	CTTTGATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTT	665
Qy	661	TCGCCTCAGTGCCCACTGTTCCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAA	720
Db	666	TCGCCTCAGTGCCCACTGTTCCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAA	725
Qy	721	CGGGTTCAATTCTGGCCGCCGGGTGACCTGGCCACCATTACGGCATGAACCGGCCCTT	780
Db	726	CGGGTTCAATTCTGGCCGCCGGGTGACCTGGCCACCATTACGGCATGAACCGGCCCTT	785
Qy	781	CCTGCTCCTCATGGCCACCCCGTGGAGAGGGCCAGCACCTGCACAGCTCCCGGCACCG	840
Db	786	CCTGCTCCTCATGGCCACCCCGTGGAGAGGGCCAGCACCTGCACAGCTCCCGGCACCG	845
Qy	841	CCGAGCCCTGGATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCCT	900
Db	846	CCGA-----GCCCT	854
Qy	901	GGATACCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTCTACAT	960
Db	855	GGATACCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTCTACAT	914
Qy	961	TGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTTCATGAACCCAAGGGCTACCATGCCAA	1020
Db	915	TGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTTCATGAACCCAAGGGCTACCATGCCAA	974
Qy	1021	TTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCTT	1080
Db	975	TTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCTT	1034
Qy	1081	GGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCCGTGCTGCGTGCCGCAGGC	1140
Db	1035	GGCTCTGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCCGTGCTGCGTGCCGCAGGC	1094

```

Qy      1141 GCTGGAGCCACTGCCCATCGTGTA TACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTC 1200
          |||
Db      1095 GCTGGAGCCACTGCCCATCGTGTA TACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTC 1154

Qy      1201 CAACATGATCGTGCGTTCCTGCAAGTGCAGCTGAGGCCCGCCCCGCCCCACAGCCCCGCC 1260
          |||
Db      1155 CAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA-GCCCCGCCCCGCCCCACAGCCCCGCC 1213

Qy      1261 CACCCGGCAGGCCCGGCCCAACCCCGCCCGCCTCACCGGGGCTGTATTTAAGGACATCG 1320
          |||
Db      1214 CACCCGGCAGGCCCGGCCCAACCCCGCCCGCCTCACCGGGGCTGTATTTAAGGACATCG 1273

Qy      1321 TGCCCCAAGCCCACTTGGGATCGATTAAAGCGGCCGCGA 1359
          |||
Db      1274 TGCCCCAAGCCCAC-TGGGATCGATTAAAGGTGGAGAGA 1311

```

RESULT 2

ABQ76674

ID ABQ76674 standard; DNA; 2527 BP.

XX

AC ABQ76674;

XX

DT 26-MAR-2003 (first entry)

XX

DE Androgen receptor signalling pathway-associated DNA E00973.

XX

KW Androgen receptor; transactivation; modulator; Smad3; Smad4; Akt; TGF-B;
KW signal transduction pathway; transforming growth factor-B; phosphatase;
KW tensin; cytostatic; antiproliferative; cellular proliferation; cancer;
KW E00973; ds.

XX

OS Synthetic.

XX

PN WO200282081-A2.

XX

PD 17-OCT-2002.

XX

PF 05-APR-2002; 2002WO-US11086.

XX

PR 06-APR-2001; 2001US-282266P.

PR 13-MAR-2002; 2002US-365060P.

XX

PA (UYRP) UNIV ROCHESTER.

XX

PI Chang C;

XX

DR WPI; 2003-046871/04.

XX

PT Modulating androgen receptor activity, by administering a compound that
PT modulates receptor activity, inhibits receptor-signal transduction
PT pathway/receptor-coactivator interaction or changes amount or receptor
PT -

XX

PS Disclosure; Page 225-226; 302pp; English.

XX

CC This invention describes a novel method for modulating androgen receptor

Qy	546	GGCGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCCGAGTGGCTGTCTTTG	605
Db	1377	GGCGATACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTG	1436
Qy	606	ATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGAGAGAGGCTATAGAGGGTTTTTCGCC	665
Db	1437	ATGTCACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTTCGCC	1496
Qy	666	TCAGTGCCCACTGTTCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGT	725
Db	1497	TTAGCGCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGT	1556
Qy	726	TCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTACGGCATGAACCGGCCCTTCTGTC	785
Db	1557	TCACTACCGGCCGCCGAGGTGACCTGGCCACCATTATGGCATGAACCGGCCTTCTGTC	1616
Qy	786	TCCTCATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAG	845
Db	1617	TTCTCATGGCCACCCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGCCGA-	1675
Qy	846	CCCTGGATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCCTGGATA	905
Db	1676	-----GCCCTGGACA	1685
Qy	906	CCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTCTACATTGACT	965
Db	1686	CCAACTATTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTGTACATTGACT	1745
Qy	966	TCCGGAAGGACCTGGGCTGGAAGTGGATTATGAACCCAAGGGCTACCATGCCAATTTCT	1025
Db	1746	TCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCAAGGGCTACCATGCCAATTTCT	1805
Qy	1026	GCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTC	1085
Db	1806	GCCTCGGGCCCTGCCCCCTACATTTGGAGCCTGGACACGAGTACAGCAAGGTCCTGGCCC	1865
Qy	1086	TGTACAACCAGCACAAACCGGGCGCGTCGGCGGCGCCGTGCTGCGTGCCGAGGCGCTGG	1145
Db	1866	TGTACAACCAGCATAAACCGGGCGCCTCGGCGGCGCCGTGCTGCGTGCCGAGGCGCTGG	1925
Qy	1146	AGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACA	1205
Db	1926	AGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGGAGCTGTCCAACA	1985
Qy	1206	TGATCGTGCGTTCTTGCAAGTGCAGCTGAGGCCCGCCCCGCCACAGCCCCGCCACCC	1265
Db	1986	TGATCGTGCGTCTCTGCAAGTGCAGCTGAGGTCCCGCCCCGCC--CCGCCCGCCCGGCC	2043
Qy	1266	GGCAGGCCCGGCCCCACCCCGCCCGCCTCACCGGGGCTGTATTTAAGGACATCGTGCCC	1325
Db	2044	CCACCCCGCCCCGCCCCGCTGCCTTGCCCATGGGGGCTGTATTTAAGGACACCGTGCCC	2103
Qy	1326	CAAGCCCACTTGGGATCGATTAAA	1349
Db	2104	CAAGCCCACTTGGGGCCCCATTAA	2127

RESULT 3

AAN60972

ID AAN60972 standard; cDNA; 2537 BP.

XX

AC AAN60972;

XX

DT 31-OCT-2002 (updated)

DT 28-OCT-1991 (first entry)

XX

DE Sequence encoding preTGF-beta.

XX

KW Transforming growth factor beta; cancer; wound healing.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT misc_structure 37..113

FT /*tag= a

FT /note= "Sequence can form stable hairpin loops"

FT CDS 842..2014

FT /*tag= b

FT mat_peptide 1676..2011

FT /*tag= c

XX

PN EP200341-A.

XX

PD 10-DEC-1986.

XX

PF 21-MAR-1986; 86EP-0302112.

XX

PR 22-MAR-1985; 85US-0715142.

PR 13-MAR-1987; 87US-0025423.

XX

PA (GETH) GENENTECH INC.

XX

PI Derynck RMA;

XX

DR WPI; 1986-326875/50.

DR P-PSDB; AAP61468.

XX

PT TGF-beta prodn. from transformed hosts - useful esp. for treating

PT wounds (J6 2/9/86).

XX

PS Disclosure; Fig 1b; 26pp; English.

XX

CC The gene product is known to stimulate cell proliferation and
 CC inhibit anchorage-dependent growth of a variety of human cancer cell
 CC lines, it is esp. useful in treatment of burns and the promotion of
 CC surface and internal wound healing. TGF-beta may be expressed from a
 CC transformed CHO cell line.

CC (Updated on 31-OCT-2002 to add missing OS field.)

XX

SQ Sequence 2537 BP; 473 A; 893 C; 739 G; 432 T; 0 other;

Query Match 72.2%; Score 982; DB 7; Length 2537;

Best Local Similarity 84.9%; Pred. No. 3e-189;

Matches 1148; Conservative 0; Mismatches 145; Indels 59; Gaps 2;

Qy	6	CCGAGATGGCGCCTTCGGGGGCTGCGGCTCTTGCCGCTGCTGCTGCCGCTGCTGTGGCTGC	65
Db	837	CCCCCATGCCGCCCTCCGGGCTGCGGCTGCTGCCGCTGCTGCTACCGCTGCTGTGGCTAC	896
Qy	66	TAGTGCTGACGCCCTGGCCGGCCGGCCCGGACTGTCCACCTGCAAGACCATCGACATGG	125
Db	897	TGGTGCTGACGCCCTGGCCCGCCGGCCCGGACTATCCACCTGCAAGACTATCGACATGG	956
Qy	126	AGCTGGTGAAGCGGAAGCGCATCGAGGCCATTTCGCGGCCAGATTCTGTCCAAGCTTCGGC	185
Db	957	AGCTGGTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGC	1016
Qy	186	TTGCCAGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGG	245
Db	1017	TCGCCAGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGCTGCCCGAGGCCGTGCTCG	1076
Qy	246	CTCTTTACAACAGTACCCGCGACCGGTTAGCCGGGGAAAGTGTGCAACCGGAGCCCCGAGC	305
Db	1077	CCCTGTACAACAGCACCCGCGACCGGTTGGCCGGGGAGAGTGCAGAACCGGAGCCCCGAGC	1136
Qy	306	CAGAGGCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACC	365
Db	1137	CTGAGGCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACG	1196
Qy	366	AAATCTATGATAAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGG	425
Db	1197	AAATCTATGACAAGTTCAAGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAG	1256
Qy	426	AGCTCCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGA	485
Db	1257	AGCTCCGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGA	1316
Qy	486	GGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCT	545
Db	1317	GGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCT	1376
Qy	546	GGCGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCCTTG	605
Db	1377	GGCGTACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTG	1436
Qy	606	ATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCC	665
Db	1437	ATGTCACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTTCGCC	1496
Qy	666	TCAGTGCCCACTGTTCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAAACGGGT	725
Db	1497	TTAGCGCCCACTGCTCCTGTGACAGAGGGATAACACACTGCAAGTGGACATCAACGGGT	1556
Qy	726	TCAATTCTGGCCGCCGGGTGACCTGGCCACCATTACGGCATGAACCGGCCCTTCCTGC	785
Db	1557	TCACTACCGGCCGCCGAGGTGACCTGGCCACCATTATGGCATGAACCGGCCCTTCCTGC	1616
Qy	786	TCCTCATGGCCACCCGCTGGAGAGGGCCAGCACCTGCACAGCTCCCGGCACCGCCGAG	845
Db	1617	TTCTCATGGCCACCCGCTGGAGAGGGCCAGCATCTGCAAAGCTCCCGGCACCGCCGA-	1675

QY	846	CCCTGGATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCCTGGATA	905
Db	1676	-----GCCCTGGACA	1685
QY	906	CCAAC TACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTCTACATTGACT	965
Db	1686	CCAAC TATTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTGTACATTGACT	1745
QY	966	TCCGGAAGGACCTGGGCTGGAAGTGGATT CATGAACCCAAGGGCTACCATGCCAATTTCT	1025
Db	1746	TCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCAAGGGCTACCATGCCAATTCT	1805
QY	1026	GCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTC	1085
Db	1806	GCCTCGGGCCCTGCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAGGTCCTGGCCC	1865
QY	1086	TGTACAACCAGCACAACCCGGGCGCGTCCGGCGGCGCCGTGCTGCGTGCCGCAGGCGCTGG	1145
Db	1866	TGTACAACCAGCATAACCCGGGCGCCTCGGCGGCGCCGTGCTGCGTGCCGCAGGCGCTGG	1925
QY	1146	AGCCACTGCCCATCGTG TACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACA	1205
Db	1926	AGCCGCTGCCCATCGTG TACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACA	1985
QY	1206	TGATCGTGCGTTCCTGCAAGTGCAGCTGAGGCCCCGCCCCGCCACAGCCCCGCCACCC	1265
Db	1986	TGATCGTGCGTTCCTGCAAGTGCAGCTGAGGTCCCCGCCCCGCCCGCCCCGCCCGGCAG	2045
QY	1266	GGCAGGCCCCGCCCCACCCCCGCCCCCT-----CACCGGGGCTGTATTTAAGGACA	1317
Db	2046	GCCCGGCCCCACCCCCGCCCCGCCCCGCTGCCTTGCCCATGGGGGCTGTATTTAAGGACA	2105
QY	1318	TCGTGCCCCAAGCCCACTTGGGATCGATTAAA	1349
Db	2106	CCGTGCCCCAAGCCCACTTGGGGCCCCATTAA	2137

RESULT 4

AAQ03301

ID AAQ03301 standard; DNA; 2537 BP.

XX

AC AAQ03301;

XX

DT 25-MAR-2003 (updated)

DT 05-AUG-1990 (first entry)

XX

DE cDNA encoding human pre-transforming growth factor-beta-1 (pre-TGF-beta-1).

XX

KW Transforming growth factor-beta-1 (TGF-beta-1);

KW neoplastic cell line inhibition;

KW EGF-potentiated anchorage-independent growth;

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 842..2014

```

FT          /*tag=  a
FT  mat_peptide  1676..2011
FT          /*tag=  b
FT  misc_difference  37..113
FT          /*tag=  c
FT          /note="stable hairpin loops"
FT  misc_feature  2015..2100
FT          /*tag=  d
FT          /note="G-C rich sequence
FT          and a downstream TATA-like sequence"
XX
PN  US4886747-A.
XX
PD  12-DEC-1989.
XX
PF  13-MAR-1987;   87US-0025423.
XX
PR  13-MAR-1987;   87US-0025423.
XX
PA  (GETH ) GENENTECH INC.
XX
PI  Derynck RMA,  Goeddel DV;
XX
DR  WPI; 1990-051338/07.
DR  P-PSDB; AAR05258.
XX
PT  Nucleic acid encoding transforming growth factor-beta -
PT  cloned into expression vectors for expression in eukaryotic host
PT  cells for therapeutic use
XX
PS  Disclosure;  Fig 1b; 28pp; English.
XX
CC  It was obtained by an analysis of several overlapping cDNAs and gene
CC  fragments, leading to the detn. of a continuous sequence corresp. to the
CC  TGF-beta-1 precursor mRNA. It is useful in constructing vectors that
CC  encode biologically active transforming growth factor (TGF-beta),
CC  operably linked to DNA that encodes a secretory leader (SL). It, or a
CC  nucleic acid capable of hybridising with it, can also be labelled and
CC  used in diagnostic assays for DNA or mRNA encoding TGF-beta or related
CC  proteins.
CC  (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ  Sequence 2537 BP; 473 A; 893 C; 739 G; 432 T; 0 other;

Query Match          72.2%;  Score 982;  DB 11;  Length 2537;
Best Local Similarity  84.9%;  Pred. No. 3e-189;
Matches 1148;  Conservative   0;  Mismatches 145;  Indels   59;  Gaps    2;

QY          6  CCGAGATGGCGCCTTCGGGGCTGCGGCTCTTGCCGCTGCTGCTGCCGCTGCTGTGGCTGC 65
              ||   ||| ||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db          837  CCCCCATGCCGCCCTCCGGGCTGCGGCTGCTGCCGCTGCTGCTACCGCTGCTGTGGCTAC 896

QY          66  TAGTGCTGACGCCTGGCCGGCCGGCCGGGACTGTCCACCTGCAAGACCATCGACATGG 125
              | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db          897  TGGTGCTGACGCCTGGCCGGCCGGCCGGGACTATCCACCTGCAAGACTATCGACATGG 956

QY          126  AGCTGGTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGC 185

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Db	957	 AGCTGGTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGC	1016
Qy	186	TTGCCAGCCCCCGAGCCAGGGGGACGTGCCGCCCGCCCGCTGCCTGAGGCAGTACTGG	245
Db	1017	TCGCCAGCCCCCGAGCCAGGGGGAGGTGCCGCCCGCCCGCTGCCCGAGGCCGTGCTCG	1076
Qy	246	CTCTTTACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTGGAACCGGAGCCCGAGC	305
Db	1077	CCCTGTACAACAGCACCCGCGACCGGGTGGCCGGGGAGAGTGCAGAACCGGAGCCCGAGC	1136
Qy	306	CAGAGGCGGACTACTACGCCAAGGAGGTACCCGCGTGCTAATGGTGGAAAGCGGCAACC	365
Db	1137	CTGAGGCCGACTACTACGCCAAGGAGGTACCCGCGTGCTAATGGTGGAAACCCACAACG	1196
Qy	366	AAATCTATGATAAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCCG	425
Db	1197	AAATCTATGACAAGTTCAAGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAG	1256
Qy	426	AGCTCCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGA	485
Db	1257	AGCTCCGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGA	1316
Qy	486	GGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCTT	545
Db	1317	GGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCTT	1376
Qy	546	GGCGCTACCTCAGCAACCGGCTGCTGGCCCCAGTGACTCACCGGAGTGGCTGTCTTTTG	605
Db	1377	GGCGATACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTG	1436
Qy	606	ATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCGAGAGGGCTATAGAGGGTTTTTCGCC	665
Db	1437	ATGTCACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTTCGCC	1496
Qy	666	TCAGTGCCCACTGTTCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGT	725
Db	1497	TTAGCGCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGT	1556
Qy	726	TCAATTCTGGCCGCCGGGTGACCTGGCCACCATTACGGCATGAACCGGCCCTTCTCTGC	785
Db	1557	TCACTACCGGCCGCCGAGGTGACCTGGCCACCATTATGGCATGAACCGGCCCTTCTCTGC	1616
Qy	786	TCCTCATGGCCACCCGCTGGAGAGGGCCAGCACCTGCACAGCTCCCGGCACCGCCGAG	845
Db	1617	TTCTCATGGCCACCCGCTGGAGAGGGCCAGCATCTGCAAAGCTCCCGGCACCGCCGA-	1675
Qy	846	CCCTGGATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCCTGGATA	905
Db	1676	-----GCCCTGGACA	1685
Qy	906	CCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTCTACATTGACT	965
Db	1686	CCAACTATTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTGTACATTGACT	1745
Qy	966	TCCGGAAGGACCTGGGCTGGAAGTGGATTATGAACCCAAGGGCTACCATGCCAATTTCT	1025

```

Db      1746 TCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCATGCCAACTTCT 1805
Qy      1026 GCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTC 1085
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1806 GCCTCGGGCCCTGCCCCCTACATTTGGAGCCTGGACACGACAGTACAGCAAGGTCCTGGCCC 1865
Qy      1086 TGTACAACCAGCACAACCCGGGCGCGTTCGGCGGCGCCGTGCTGCGTGCCGCAGGCGCTGG 1145
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Db      1866 TGTACAACCAGCATAACCCGGGCGCCTCGGCGGCGCCGTGCTGCGTGCCGCAGGCGCTGG 1925
Qy      1146 AGCCACTGCCCATCGTGTAATACTGAGTGGGCGCAAGCCCAAGGTGGAGCAGCTGTCCAACA 1205
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Db      1926 AGCCGCTGCCCATCGTGTAATACTGAGTGGGCGCAAGCCCAAGGTGGAGCAGCTGTCCAACA 1985
Qy      1206 TGATCGTGCGTTCTTGCAAGTGCAGCTGAGGCCCCGCCCCGCCCCACAGCCCCGCCCCACCC 1265
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Db      1986 TGATCGTGCGTTCTTGCAAGTGCAGCTGAGGTCCCCGCCCCGCCCCGCCCCGCCCCGGCAG 2045
Qy      1266 GGCAGGCCCCGCCCCACCCCCGCCCCGCT-----CACCGGGGCTGTATTTAAGGACA 1317
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Qy      1318 TCGTGCCCCAAGCCCACTTGGGATCGATTAAA 1349
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Db      2106 CCGTGCCCCAAGCCCACTTGGGGCCCCATTAA 2137

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RESULT 5

AAQ02814

ID AAQ02814 standard; cDNA; 2537 BP.

XX

AC AAQ02814;

XX

DT 25-MAR-2003 (updated)

DT 31-OCT-2002 (updated)

DT 31-MAY-1989 (first entry)

XX

DE Sequence of pre-TGF-beta1 cDNA.

XX

KW Transforming growth factor beta-3 (TGF beta 3); tumour cells; growth inhibition.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 842..2011

FT /*tag= a

FT /label=pre-TGF beta 1

FT CDS 1677..2011

FT /*tag= b

FT /label=mature TGF-beta 1

FT GC_signal 2015..2092

FT /*tag= c

FT misc_feature 2093..2099

FT /*tag= d

FT /label=TATA-like sequence

FT stem_loop 37..113

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FT          /*tag= e
FT  misc_feature  863..911
FT          /*tag= f
FT          /label=hydrophobic domain
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PN WO8912101-A.

PD 14-DEC-1989.

PF 08-JUN-1988; 88WO-US01945.

PR 08-JUN-1988; 88WO-US01945.

PA (GETH) GENENTECH INC.

PI DERNYCK RMA, GOEDDEL DV;

DR WPI; 1990-007474/01.

DR P-PSDB; AAR04034.

PT Nucleotide sequence encoding transforming growth factor beta-3 -used as a
PT probe, or to produce TGF beta 3, for growth inhibition of certain normal
PT and neoplastic cells, eg A549.

PS Disclosure; Fig. 1b; 61pp; English.

Sequence encodes the 390 amino acid (AA) precursor transforming growth factor-beta 1 (pre-TGF-beta 1) polypeptide. The 5' untranslated region of the TGF-beta 1 mRNA is 841 bases long, is purine rich and has a region of potential secondary structure. The TATA-like sequence in the 3' untranslated region of the gene is presumably a polyadenylation signal. Mature TGF-beta 1 comprises the C-terminal 112 AA's of pre-TGF-beta 1 and is cleaved at the Arg-Arg dipeptide preceding its NH2 terminus. The nucleic acid encoding the second subtype of TGF-beta (TGF-beta 3) is useful as a probe or to produce TGF-beta 3 for inhibition of growth of normal and neoplastic cells.

CC (Updated on 31-OCT-2002 to add missing OS field.)

CC (Updated on 25-MAR-2003 to correct PR field.)

CC (Updated on 25-MAR-2003 to correct PI field.)

SO Sequence 2537 BP; 473 A; 893 C; 739 G; 432 T; 0 other;

Query Match 72.2%; Score 982; DB 11; Length 2537;

Best Local Similarity 84.9%; Pred. No. 3e-189;

Matches 1148; Conservative 0; Mismatches 145; Indels 59; Gaps 2;

QY 6 CCGAGATGGCGCCTTCGGGGCTGCGGCTCTTGCCGCTGCTGCTGCCGCTGCTGTGGCTGC 65

Db 837 CCCCCATGCCGCCCTCCGGGCTGCGGCTGCTGCCGCTGCTGCTACCGCTGCTGTGGCTAC 896

Qy 66 TAGTGCTGACGCCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGG 125

Db 897 TGGTGCTGACGCCTGGCCCCGCCGGCCGCGGGACTATCCACCTGCAAGACTATCGACATGG 956

Qy 126 AGCTGGTGAAGCGGAAGCGCATCGAGGCCATTGCGGCCAGATTCTGTCCAAGCTTCGGC 185

Db 957 AGCTGGTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGC 1016

Qy	186	TTGCCAGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGG	245
Db	1017	TCGCCAGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGCTGCCCGAGGCCGTGCTCG	1076
Qy	246	CTCTTTACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTGCAACCGGAGCCCGAGC	305
Db	1077	CCCTGTACAACAGCACCCGCGACCGGGTGGCCGGGGAGAGTGCAGAACCGGAGCCCGAGC	1136
Qy	306	CAGAGGCGGACTACTACGCCAAGGAGGTCAACCGCGTGCTAATGGTGGAAAGCGGCAACC	365
Db	1137	CTGAGGCCGACTACTACGCCAAGGAGGTCAACCGCGTGCTAATGGTGGAAACCCACAACG	1196
Qy	366	AAATCTATGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCCG	425
Db	1197	AAATCTATGACAAGTTCAAGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAG	1256
Qy	426	AGCTCCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGA	485
Db	1257	AGCTCCGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGA	1316
Qy	486	GGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCTT	545
Db	1317	GGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCTT	1376
Qy	546	GGCGCTACCTCAGCAACCGGCTGCTGGCCCCAGTGACTACCGGAGTGGCTGTCCTTTG	605
Db	1377	GGCGATACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTG	1436
Qy	606	ATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGAGAGAGGCTATAGAGGGTTTTCGCC	665
Db	1437	ATGTCACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTTCGCC	1496
Qy	666	TCAGTGCCCACTGTTCTCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGT	725
Db	1497	TTAGCGCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGT	1556
Qy	726	TCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTACCGGCATGAACCGGCCCTTCTTGC	785
Db	1557	TCACTACCGGCCGCCGAGGTGACCTGGCCACCATTATGGCATGAACCGGCCCTTCTTGC	1616
Qy	786	TCCTCATGGCCACCCCGCTGGAGAGGGCCAGCACCTGCACAGCTCCCGGCACCGCCGAG	845
Db	1617	TTCTCATGGCCACCCCGCTGGAGAGGGCCAGCATCTGCAAAGCTCCCGGCACCGCCGA-	1675
Qy	846	CCCTGGATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCCTGGATA	905
Db	1676	-----GCCCTGGACA	1685
Qy	906	CCAATACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTCTACATTGACT	965
Db	1686	CCAATAATTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTGTACATTGACT	1745
Qy	966	TCCGGAAGGACCTGGGCTGGAAGTGGATTATGAACCCAAGGGCTACCATGCCAATTTCT	1025
Db	1746	TCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCATGCCAATTTCT	1805

Qy	1026	GCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTC	1085
Db	1806	GCCTCGGGCCCTGCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAGGTCCTGGCCC	1865
Qy	1086	TGTACAACCAGCACAAACCGGGCGCGTCGGCGGCGCCGTGCTGCGTGCCGCAGGCGCTGG	1145
Db	1866	TGTACAACCAGCATAAACCGGGCGCCTCGGCGGCGCCGTGCTGCGTGCCGCAGGCGCTGG	1925
Qy	1146	AGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACA	1205
Db	1926	AGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACA	1985
Qy	1206	TGATCGTGCGTTCTTGCAAGTGCAGCTGAGGCCCCGCCCCGCCACAGCCCCGCCACCC	1265
Db	1986	TGATCGTGCGTCTCTGCAAGTGCAGCTGAGGTCCCGCCCCGCCCGCCCCGCCCGGCGAG	2045
Qy	1266	GGCAGGCCCCGGCCCCACCCCCGCCCCCT-----CACCGGGGCTGTATTTAAGGACA	1317
Db	2046	GCCCCGCCCCACCCCCGCCCCGCCCCGCTGCCTTGCCCATGGGGGCTGTATTTAAGGACA	2105
Qy	1318	TCGTGCCCCAAGCCCACTGGGATCGATTAAA	1349
Db	2106	CCGTGCCCCAAGCCCACTGGGGCCCCATTAA	2137

AAT15720

XX

XX

DT 24-JUL-1997 (revised)

XX

XX

KW recombinant production; ss.

OS

FT 5'UTR 1..841

FT	misc feature	37..113
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FT CDS 842..2014

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 FT /*tag= e
 FT /note= "GC-rich region; possibly responsible for the
 FT fact 3'UTR of mRNA could not be cloned as cDNA;
 FT may be important for transcription efficiency"
 FT repeat_unit 2019..2023
 FT /*tag= f
 FT TATA_signal 2094..2100
 FT /*tag= g
 FT /note= "TATA-like sequence; no evidence that this
 FT functions a promoter"
 FT polyA_signal 2514..2520
 FT /*tag= h
 FT misc_signal 2529..2536
 FT /*tag= i
 FT /note= "consensus sequence immediately precedes
 FT polyA-tail (Benoist et al)"
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 PN US5482851-A.
 XX
 PD 09-JAN-1996.
 XX
 PF 05-NOV-1993; 93US-0147364.
 XX
 PR 13-MAR-1987; 87US-0025423.
 PR 22-MAR-1985; 85US-0715142.
 PR 04-AUG-1989; 89US-0389929.
 PR 04-MAR-1992; 92US-0845893.
 PR 05-NOV-1993; 93US-0147364.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Derynck RMA, Goeddel DV;
 XX
 DR WPI; 1996-076891/08.
 DR P-PSDB; AAR90827.
 XX
 PT New recombinant human transforming growth factor-beta prods. - produced
 PT using Chinese hamster ovary cells, for use in diagnostic applications
 PT or in therapy
 XX
 PS Example 3; Fig 1; 26pp; English.
 XX
 CC The cDNA encodes the pre-transforming growth factor (TGF) beta 1 protein.
 CC The nucleotide sequence was obt'd. by an analysis of several overlapping
 CC cDNAs and gene fragments. The DNA is useful for the recombinant
 CC production of TGF beta 1, which can be used in, e.g. wound healing.
 CC (Revised entry submitted to correct sequence analysis breakdown.)
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 2537 BP; 473 A; 893 C; 739 G; 432 T; 0 other;

Query Match 72.2%; Score 982; DB 17; Length 2537;
 Best Local Similarity 84.9%; Pred. No. 3e-189;
 Matches 1148; Conservative 0; Mismatches 145; Indels 59; Gaps 2;

Qy 6 CCGAGATGGCGCCTTCGGGGCTGCGGCTCTTGCCGCTGCTGCTGCCGCTGCTGTGGCTGC 65

Db	837	CCCCCATGCCGCCCTCCGGGCTGCCGGCTGCTGCCGCTGCTGCTACCGCTGCTGTGGCTAC	896
Qy	66	TAGTGCTGACGCCTGGCCGGCCGGCCGGGACTGTCCACCTGCAAGACCATCGACATGG	125
Db	897	TGGTGCTGACGCCTGGCCCGCCGGCCGGGACTATCCACCTGCAAGACTATCGACATGG	956
Qy	126	AGCTGGTGAAGCGGAAGCGCATCGAGGCCATTCCGCGGCCAGATTCTGTCCAAGCTTCGGC	185
Db	957	AGCTGGTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGC	1016
Qy	186	TTGCCAGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCGCTGCCTGAGGCAGTACTGG	245
Db	1017	TCGCCAGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCGCTGCCCGAGGCCGTGCTCG	1076
Qy	246	CTCTTTACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTGAAACCGGAGCCCGAGC	305
Db	1077	CCCTGTACAACAGCACCCGCGACCGGGTGGCCGGGGAGAGTGCAGAAACCGGAGCCCGAGC	1136
Qy	306	CAGAGGCGGACTACTACGCCAAGGAGGTCACCCCGCTGCTAATGGTGGAAGCGGCAACC	365
Db	1137	CTGAGGCCGACTACTACGCCAAGGAGGTCACCCCGCTGCTAATGGTGGAACCCACAACG	1196
Qy	366	AAATCTATGATAAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCCG	425
Db	1197	AAATCTATGACAAGTTCAAGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAG	1256
Qy	426	AGTCCCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGA	485
Db	1257	AGTCCGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGA	1316
Qy	486	GGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCTT	545
Db	1317	GGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCTT	1376
Qy	546	GGCGTACCTCAGCAACCGGCTGCTGGCCCCAGTGACTCACCGGAGTGCGTGTCTTTTG	605
Db	1377	GGCGATACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGTTATCTTTTG	1436
Qy	606	ATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGAGAGAGGCTATAGAGGGTTTTTCGCC	665
Db	1437	ATGTCACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTTCGCC	1496
Qy	666	TCAGTGCCCACTGTTCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGT	725
Db	1497	TTAGCGCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGACATCAACGGGT	1556
Qy	726	TCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCTCTGC	785
Db	1557	TCACTACCGGCCGCCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCCTTCTCTGC	1616
Qy	786	TCCTCATGGCCACCCCGCTGGAGAGGGCCAGCACCTGCACAGCTCCCGGCACCGCCGAG	845
Db	1617	TTCTCATGGCCACCCCGCTGGAGAGGGCCAGCATCTGCAAAGCTCCCGGCACCGCCGA-	1675
Qy	846	CCCTGGATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCCTGGATA	905

```

Db      1676 -----GCCCTGGACA 1685
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Db      1686 CCAACTATTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTGTACATTGACT 1745
Qy      966 TCCGGAAGGACCTGGGCTGGAAGTGGATTCATGAACCCAAGGGCTACCATGCCAATTTCT 1025
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Db      1746 TCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCATGCCAATTCT 1805
Qy      1026 GCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTC 1085
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Qy      1086 TGTACAACCAGCACAAACCGGGCGCGTCCGGCGGCGCCGTGCTGCGTGCCGCAGGCGCTGG 1145
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Qy      1146 AGCCACTGCCCATCGTGTA TACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACA 1205
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Db      1986 TGATCGTGCGTCTCTGCAAGTGCAGCTGAGGTCCCGCCCCGCCCCGCCCCGCCCCGGCAG 2045
Qy      1266 GGCAGGCCCCGCCCCACCCCCGCCCCGCT-----CACCGGGGCTGTATTTAAGGACA 1317
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Db      2046 GCCCGGCCCCACCCCCGCCCCGCCCCGCTGCTTGCCCATGGGGGCTGTATTTAAGGACA 2105
Qy      1318 TCGTGCCCCAAGCCCACTTGGGATCGATTAAA 1349
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RESULT 7

AAQ56923

ID AAQ56923 standard; cDNA; 2537 BP.

XX

AC AAQ56923;

XX

DT 25-MAR-2003 (updated)

DT 09-JUL-1994 (first entry)

XX

DE Human pre-TGF-beta-1.

XX

KW TGF-beta-1; TGF-beta-2; transforming growth factor beta-1;

KW transforming growth factor beta-3; recombinant; wound healing;

KW vulnerary; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

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FT /note= "possible hairpin loop region"

FT CDS 842..2014

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PN US5284763-A.

PD 08-FEB-1994.

PF 04-MAR-1992: 92US-0845893.

PR 22-MAR-1985; 85US-0715142.

PR 13-MAR-1987; 87US-0025423.

PR 04-AUG-1989; 89US-0389929.

PR 04-MAR-1992; 92US-0845893.

PA (GETH) GENENTECH INC.

PI Derynk RMA, Goeddel DV;

DR WPI; 1994-056343/07.

DR P-PSDB; AAR46227.

PT Nucleic acid sequences encoding transforming growth factor-beta -
PT diagnostic probes, and for use in therapeutics

PS Disclosure; Fig 1b; 25pp; English.

CC cDNA sequences were determined for human pre-TGF-beta-1 (AAQ56923),
CC pig TGF-beta-3 (AAQ56925) and human TGF-beta-3 (AAQ56926), and the
CC corresponding amino acid sequences were determined (AAR46227-29,
CC respectively). A genomic fragment corresponding to a human TGF-
CC beta-1 exon (AAQ56924) was also isolated and its amino acid sequence
CC determined (AAR46230). The sequences have been used in the
CC construction of vectors for the expression of recombinant TGF-
CC beta.

CC (Updated on 25-MAR-2003 to correct PF field.)

SQ Sequence 2537 BP; 473 A; 890 C; 742 G; 432 T; 0 other;

Query Match 72.0%; Score 980.4; DB 15; Length 2537;
Best Local Similarity 84.8%; Pred. No. 6.2e-189;
Matches 1147; Conservative 0; Mismatches 146; Indels 59; Gaps 2;

Qy 6 CCGAGATGGCGCCTTCGCGGCTGCGGCTCTTGCCGCTGTGCTGCCGCTGTGTGGCTGC 65
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Db 837 CCCCCATGCCGCCCTCCGGGCTGCGGCTGTGCGGCTGTGCTACCGCTGTGTGGCTAC 896

Qy 66 TAGTGCTGACGCCTGGCCGGCCGGCCGCCGACTGTCCACCTGCAAGACCATCGACATGG 125
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Qy 126 AGCTGGTGAAGCGGAAGCGCATCGAGGCCATTGCGGCCAGATTCTGTCCAAGCTTCGGC 185
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Db 957 AGCTGGTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGC 1016

Qy	186	TTGCCAGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCCTGAGGCAGTACTGG	245
Db	1017	TCGCCAGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGCTGCCCGAGGCCGTGCTCG	1076
Qy	246	CTCTTTTACAACAGTACCCGCGACCGGGTAGCCGGGGAAAAGTGTGCAACCGGAGCCCGAGC	305
Db	1077	CCCTGTACAACAGCACCCGCGACCGGGTGGCCGGGGAGAGTGCAGAACGGGAGCCCGAGC	1136
Qy	306	CAGAGGCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAGCGGCAACC	365
Db	1137	CTGAGGCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAACCCACAACG	1196
Qy	366	AAATCTATGTATAAATTCAGGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGG	425
Db	1197	AAATCTATGACAAGTTCAGAGCAGGTACACACAGCATATATATGTTCTTCAACACATCAG	1256
Qy	426	AGCTCCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGA	485
Db	1257	AGCTCCGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGCAGAGCTGCGTCTGCTGA	1316
Qy	486	GGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCT	545
Db	1317	GGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCT	1376
Qy	546	GGCGCTACCTCAGCAACCGGCTGCTGGCCCCAGTGACTCACCGGAGTGGCTGTCCTTTG	605
Db	1377	GGCGATACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTG	1436
Qy	606	ATGTCAACGGAGTTGTGCGGCAGTGGCTGACCCGAGAGAGGCTATAGAGGGTTTTTCGCC	665
Db	1437	ATGTCAACGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTTCGCC	1496
Qy	666	TCAGTGCCCACTGTTTCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGT	725
Db	1497	TTAGCGCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGACATCAACGGGT	1556
Qy	726	TCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTACGGCATGAACCGGCCCTTCTGTC	785
Db	1557	TCACTACCGGCCGCCGAGGTGACCTGGCCACCATTATGGCATGAACCGGCCCTTCTGTC	1616
Qy	786	TCCTCATGGCCACCCCGCTGGAGAGGGCCAGCACCTGCACAGCTCCCGGCACCGCCGAG	845
Db	1617	TTCTCATGGCCACCCCGCTGGAGAGGGCCAGCATCTGCAAAGCTCCCGGCACCGCCGA-	1675
Qy	846	CCCTGGATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCCTGGATA	905
Db	1676	-----GCCCTGGACA	1685
Qy	906	CCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTCTACATTGACT	965
Db	1686	CCAACTATTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTGTACATTGACT	1745
Qy	966	TCCGGAAGGACCTGGGCTGGAAGTGATTATGAACCCAAGGGCTACCATGCCAATTTCT	1025
Db	1746	TCCGCAAGGACCTCGGCTGGAAGTGATCCACGAGCCAAGGGCTACCATGCCAATTCT	1805
Qy	1026	GCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTC	1085

Db	1806	GCCTCGGGCCCTGCCCTACATTGGAGCCTGGACACGCAGTACAGCAAGGTCCTGGCCC	1865
Qy	1086	TGTACAACCAGCACAAACCGGGCGCGTCGGCGGCGCCGTGCTGCGTGCCGCAGGCGCTGG	1145
Db	1866	TGTACAACCAGCATAAACCGGGCGCCTCGGCGGCGCCGTGCTGCGTGCCGCAGGCGCTGG	1925
Qy	1146	AGCCACTGCCCATCGTGTA	1205
Db	1926	AGCCGCTGCCCATCGTGTA	1985
Qy	1206	TGATCGTGCGTTCCTGCAAGTGCAGCTGAGGCCCCGCCCCGCCACAGCCCCGCCACCC	1265
Db	1986	TGATCGTGCGTTCCTGCAAGTGCAGCTGAGGTCCCGCCCCGCCCCGCCCCGCCCCGGCAG	2045
Qy	1266	GGCAGGCCCGGCCCCACCCCCGCCCCGCT-----CACCGGGGCTGTATTTAAGGACA	1317
Db	2046	GCCCGGCCCCACCCCCGCCCCGCCCCGCTTGCCCATGGGGGCTGTATTTAAGGACA	2105
Qy	1318	TCGTGCCCCAAGCCCACTTGGGATCGATTAAA	1349
Db	2106	CCGTGCCCCAAGCCCACTTGGGGCCCCATTAA	2137

RESULT 8

AAV52933

ID AAV52933 standard; cDNA; 2537 BP.

XX

AC AAV52933;

XX

DT 25-MAR-2003 (updated)

DT 21-DEC-1998 (first entry)

XX

DE Human pre-transforming growth factor-beta 1 cDNA.

XX

KW Transforming growth factor-beta 1; TGF-beta 1; human; ss.

XX

05 Homo sapiens.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT CDS 842..2014

FT /*tag= a

FT mat peptide 1676..2011

```
FT                               /*tag=  b
```

FT	stem_loop	37..113
----	-----------	---------

FT /*tag= b

```
FT      /note= "putative stable hairpin loop"
```

```
FT    misc_feature    2015..2100
```

FT /*tag= c

```
FT                               /note= "GC-rich sequence"
```

FT	polyA_signal	2514..2520
----	--------------	------------

FT /*tag= d

XX

PN US5801231-A.

XX

PD 01-SEP-1998.

XX

PF 30-MAY-1995; 95US-0454468.
XX
PR 13-MAR-1987; 87US-0025423.
PR 22-MAR-1985; 85US-0715142.
PR 04-AUG-1989; 89US-0389929.
PR 04-MAR-1992; 92US-0845893.
PR 05-NOV-1993; 93US-0147364.
PR 30-MAY-1995; 95US-0454468.

XX

PA (GETH) GENENTECH INC.

XX

PI Derynck RMA, Goeddel DV;

XX

DR WPI; 1998-494840/42.

DR P-PSDB; AAW78785.

XX

PT DNA encoding transforming growth factor-beta precursor sequence -
PT useful for analysis to perform manipulations to increase yield of
PT recombinant production of the protein

XX

PS Example 3; Fig 1B 1-3; 26pp; English.

XX

CC This nucleotide sequence codes for the human transforming growth
CC factor-beta 1 precursor (preTGF-beta 1, see AAW78785). It is a
CC composite of overlapping cDNA clones isolated from different cDNA
CC libraries (placenta, A172 glioblastoma, HT1080 fibroblastoma) using
CC TGF-beta exon (see AAV52936) restriction fragments as probes.
CC The 3' region of the sequence was determined using cloned genomic
CC DNA. The invention relates to the recombinant production of
CC TGF-beta. Biologically active TGF-beta is defined as being capable
CC of inducing EGF-potentiased anchorage independent growth of target
CC cell lines and/or growth inhibition of neoplastic cell lines.
CC Nucleic acids encoding TGF-beta have been isolated and cloned into
CC vectors which are replicated in bacteria and expressed in
CC eukaryotic cells. TGF-beta recovered from transformed cells is
CC used in known therapeutic applications. TGF-beta nucleic acids are
CC also useful in diagnosis and identification of TGF-beta clones.
CC (Updated on 25-MAR-2003 to correct PF field.)

XX

SQ Sequence 2537 BP; 475 A; 895 C; 736 G; 431 T; 0 other;

Query Match 71.8%; Score 977.2; DB 19; Length 2537;
Best Local Similarity 84.7%; Pred. No. 2.8e-188;
Matches 1145; Conservative 0; Mismatches 148; Indels 59; Gaps 2;

Qy 6 CCGAGATGGCGCCTTCGGGGCTGCGGCTCTTGCCGCTGCTGCTGCCGCTGCTGTGGCTGC 65
|| ||| |||| || ||||||||||| ||||||||||| ||||||||||| ||
Db 837 CCCCCATGCCGCCCTCCGGGCTGCGGCTGCTGCCGCTGCTGCTACCGCTGCTGTGGCTAC 896

Qy 66 TAGTGCTGACGCCTGGCCGGCCGGCCGGGACTGTCCACCTGCAAGACCATCGACATGG 125
| ||||||||||||||| ||||||| ||||||| ||||||| ||||||| ||
Db 897 TGGTGCTGACGCCTGGCCCGCCGGCCCCGGGACTATCCACCTGCAAGACTATCGACATGG 956

Qy 126 AGCTGGTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGC 185
||| ||||||||||||||| ||||||| ||||||| ||||||| |||||
Db 957 AGCAGGTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGC 1016

Qy	186	TTGCCAGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTTGAGGCAGTACTGG	245
Db	1017	TCGCCAGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGCTGCCCGAGGCCGTGCTCG	1076
Qy	246	CTCTTTTACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTGCAACCGGAGCCCGAGC	305
Db	1077	CCCTGTACAACAGCACCCGCGACCGGGTGGCCGGGGAGAGTGCAGAACCGGAGCCCGAGC	1136
Qy	306	CAGAGGCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAGCGGCAACC	365
Db	1137	CTGAGGCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAACCCACAACG	1196
Qy	366	AAATCTATGATAAAATTCAGGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGG	425
Db	1197	AAATCTATGACAAGTTCAGGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAG	1256
Qy	426	AGCTCCGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGA	485
Db	1257	AGCTCCGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGCAGAGCTGCGTCTGCTGA	1316
Qy	486	GGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCT	545
Db	1317	GGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCT	1376
Qy	546	GGCGCTACCTCAGCAACCGGCTGCTGGCCCCAGTGACTCACCGGAGTGGCTGTCCTTTG	605
Db	1377	GGCGATACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTG	1436
Qy	606	ATGTCAACCGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCC	665
Db	1437	ATGTCAACCGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGAGAAATTGAGGGCTTTTCGCC	1496
Qy	666	TCAGTGCCCACTGTTTCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGT	725
Db	1497	TTAGCGCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGT	1556
Qy	726	TCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTACGGCATGAACCGGCCCTTCTGTC	785
Db	1557	TCACTACCGGCCGCCGAGGTGACCTGGCCACCATTATGGCATGAACCGGCCTTCTGTC	1616
Qy	786	TCCTCATGGCCACCCCGCTGGAGAGGGGCCAGCACCTGCACAGCTCCCGGCACCGCCGAG	845
Db	1617	TTCTCATGGCCACCCCGCTGGAGAGGGGCCAGCATCTGCAAAGCTCCCGGCACCGCCGA-	1675
Qy	846	CCCTGGATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCCTGGATA	905
Db	1676	-----GCCCTGGACA	1685
Qy	906	CCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTCTACATTGACT	965
Db	1686	CCAACTATTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTGTACATTGACT	1745
Qy	966	TCCGGAAGGACCTGGGCTGGAAGTGGATTTCATGAACCCAAGGGCTACCATGCCAATTCT	1025
Db	1746	TCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCAAGGGCTACCATGCCAATTCT	1805
Qy	1026	GCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTC	1085

Db	1806	GCCTCGGGCCCTGCCCTACATTGAGCCTGGACACGCAGTACAGCAAGGTCCTGGCCC	1865
Qy	1086	TGTACAACCAGCACAAACCGGGCGCGTCGGCGGCGCCGTGCTGCGTGCCGCAGGCGCTGG	1145
Db	1866	TGTACAACCAGCATAAACCGGGCGCCTCGGCGGCGCCGTGCTGCGTGCCGCAGGCGCTGG	1925
Qy	1146	AGCCACTGCCCATCGTGTA	1205
Db	1926	AGCCGCTGCCCATCGTGTA	1985
Qy	1206	TGATCGTGCGTTCCTGCAAGTGCAGCTGAGGCCCGCCCCGCCACAGCCCCGCCACCC	1265
Db	1986	TGATCGTGCGCTCCTGCAAGTGCAGCTGAGGTCCCGCCCCGCCCGCCCCGCCCGGCAG	2045
Qy	1266	GGCAGGCCCGGCCCCACCCCCGCCCGCCT-----CACCGGGGCTGTATTTAAGGACA	1317
Db	2046	GCCCGGCCCCACCCCGCCCCGCCCGCCTTGCCCATGGGGGCTGTATTTAAGGACA	2105
Qy	1318	TCGTGCCCCAAGCCCACTGGGATCGATTAAA	1349
Db	2106	CCGTGCCCCAAGCCCACTGGGGCCCCATTAA	2137

RESULT 9

AA003268

ID AAQ03268 standard; DNA; 1561 BP.

XX

AC AAQ03268;

XX

DT 25-MAR-2003 (updated)

DT 12-AUG-1990 (first entry)

XX

DE Simian transforming growth factor-beta cDNA.

XX

KW Transforming growth factor-beta; psoriasis; TGF-beta; ss.

XX

OS Monkey.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT	sig peptide	283..324
----	-------------	----------

```
FT                               /*tag=  a
```

FT	mat_peptide	1096..1431
----	-------------	------------

```
FT                               /*tag=  b
```

FT /product=human transforming growth factor-beta

XX

PN EP353772-A.

XX

PD 07-FEB-1990.

XX

PF 04-AUG-1989; 89EP-0114458.

XX

PR 05-AUG-1988; 88US-0229133.

XX

PA (ONCO) ONCOGEN LP.

XX

PI Twardzik DR, Purchio AF, Ranchalis JE, Stevens V;

XX
DR WPI; 1990-038499/06.
DR P-PSDB; AAR03743.
XX
PT Inhibition of proliferation of epidermal cells -
PT used to treat psoriasis by contacting cells with compositions
PT containing transforming growth factor-beta.
XX
PS Disclosure; fig 1; 20pp; English.
XX
CC TGF-beta may be used in the treatment of hyperplasia
CC associated with acanthosis-categorised skin diseases, and
CC in alleviating psoriatic symptoms associated with cytokine-
CC induced phenomena. See also AAQ03269 and AAR03750.
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 1561 BP; 301 A; 547 C; 446 G; 267 T; 0 other;

Query Match 71.6%; Score 974.2; DB 11; Length 1561;
Best Local Similarity 85.0%; Pred. No. 1.1e-187;
Matches 1150; Conservative 0; Mismatches 143; Indels 60; Gaps 3;

Qy	6	CCGAGATGGCGCCTTCGGGGCTGCGGCTCTTGCCGCTGCTGCTGCCGCTGCTGTGGCTGC	65
Db	257	CCCCATGCCGCCCTCCGGGCTGCGGCTGCTGCCGCTGCTGCTACCGCTGCTGTGGCTAC	316
Qy	66	TAGTGCTGACGCCTGGCCGGCCGGCCGCCGACTGTCCACCTGCAAGACCATCGACATGG	125
Db	317	TGGTGCTGACGCCTAGCCGGCCGGCCGAGGACTATCCACCTGCAAGACTATCGACATGG	376
Qy	126	AGCTGGTGAAGCGGAAGCGCATCGAGGCCATTGCGGGCCAGATTCTGTCCAAGCTTCGGC	185
Db	377	AGCTGGTGAAGCGGAAGCGCATCGAGACCATCCGCGGCCAGATCCTGTCCAAGCTGCGGC	436
Qy	186	TTGCCAGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGG	245
Db	437	TCGCCAGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGCTGCCCGAGGCCGTGCTCG	496
Qy	246	CTCTTTACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTGCAACCGGAGCCCGAGC	305
Db	497	CCCTGTACAACAGCACCCGCGACCGGGTGGCCGGGGAGAGTGCGGAGCCGGAGCCCGAAC	556
Qy	306	CAGAGGCGGACTACTACGCCAAGGAGGTCACCCGGTGCTAATGGTGGAAAGCGGCAACC	365
Db	557	CGGAGGCCGACTACTACGCCAAGGAGGTCACCCGGTGCTAATGGTGGAAACCCACAACG	616
Qy	366	AAATCTATGATAAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTGCG	425
Db	617	AAATCTATGACAAGTTCAAGCAGAGCACACACAGCATATATATGTTCTTCAACACATCAG	676
Qy	426	AGCTCCGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGA	485
Db	677	AGCTCCGAGAAGCAGTACCTGAACCTGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGA	736
Qy	486	GGCTCAAGTTAAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCT	545
Db	737	GGCTCAAGTTAAAAAGTGGAGCAGCATGTGGAGCTGTACCAGAAATACAGCAACAATTCT	796

QY 546 GCGCTACCTCAGCAACCGGCTGCTGGCCCCAGTGA CTACCGGAGTGGCTGTCCTTTG 605
 |||| |||||
 Db 797 GCGGATACCTCAGCAACCGGCTGCTGGCGCCAGCAACTCGCCGGAGTGGTTGTCTTTTG 856
 QY 606 ATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTTCGCC 665
 |||||
 Db 857 ATGTCACCGGAGTTGTGCGGCAGTGGTTGAGCCGCGGAGGGGAAATTGAGGGCTTTTCGCC 916
 QY 666 TCAGTGCCCACTGTTCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGT 725
 |||||
 Db 917 TTAGCGCCCACTGCTCCTGTGACAGCAAAGATAACACACTGCAAGTGGACATCAACGGGT 976
 QY 726 TCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTACGGCATGAACCGGCCCTTCTCTGC 785
 |||||
 Db 977 TCACTACCGGCCGCCGAGGTGACCTGGCCACAATTATGTCATGAACCGGCCCTTCTCTGC 1036
 QY 786 TCCTCATGGCCACCCCGCTGGAGAGGGCCAGCACCTGCACAGCTCCCGGCACCGCCGAG 845
 |||||
 Db 1037 TTCTCATGGCCACCCCACTGGAGAGGGCCCAACATCTGCAAAGCTCCCGGCACCGCCGA- 1095
 QY 846 CCCTGGATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCCTGGATA 905
 |||||
 Db 1096 -----GCCCTGGACA 1105
 QY 906 CCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTCTACATTGACT 965
 |||||
 Db 1106 CCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTGTATATTGACT 1165
 QY 966 TCCGGAAGGACCTGGGCTGGAAGTGGATTATGAACCCAAGGGCTACCATGCCAATTTCT 1025
 |||||
 Db 1166 TCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCATGCCAATTTCT 1225
 QY 1026 GCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTC 1085
 |||||
 Db 1226 GCCTGGGGCCCTGTCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAGGTCCTGGCCC 1285
 QY 1086 TGTACAACCAGCACAACCCGGGCGCGTCCGGCGCGCCGTGCTGCGTGCCGAGGCGCTGG 1145
 |||||
 Db 1286 TGTACAACCAGCATAACCCGGGCGCCTCGGCGGCGCCGTGCTGCGTGCCGAGGCGCTGG 1345
 QY 1146 AGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACA 1205
 |||||
 Db 1346 AGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACA 1405
 QY 1206 TGATCGTGCGTTCTTGCAAGTGACAGCTGAGGCCCCGCCCCGCCACAGCCCCGCCACCC 1265
 |||||
 Db 1406 TGATCGTGCGTCTCTGCAAATGACAGCTGAGGCCCCGCCCCGCCACAGCCCCGCCACCCGGCAG 1465
 QY 1266 GGCAGGCCCCGCCCCACCCCCGCCCCCT-----CACCGGGGCTGTATTTAAGGACA 1317
 |||||
 Db 1466 GCCCGCCCCGCCCCACCCCCGCCCCCTGTCTTGCCCTTGGGGGCTGTATTTAAGGACA 1525
 QY 1318 -TCGTGCCCCAAGCCCACTTGGGATCGATTAAA 1349
 |||||
 Db 1526 CCCGTGCCCCAAGCCCACTTGGGGCCCCATTAA 1558

RESULT 10

AAI58342

ID AAI58342 standard; cDNA; 2742 BP.

XX

AC AAI58342;

XX

DT 22-OCT-2001 (first entry)

XX

DE Human polynucleotide SEQ ID NO 545.

XX

KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;

KW peripheral nervous system; neuropathy; central nervous system; CNS;

KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;

KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;

KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;

KW leukaemia; ss.

XX

OS Homo sapiens.

XX

PN WO200153312-A1.

XX

PD 26-JUL-2001.

XX

PF 26-DEC-2000; 2000WO-US34263.

XX

PR 21-JAN-2000; 2000US-0488725.

PR 25-APR-2000; 2000US-0552317.

PR 09-JUL-2000; 2000US-0598042.

PR 19-JUL-2000; 2000US-0620312.

PR 03-AUG-2000; 2000US-0653450.

PR 14-SEP-2000; 2000US-0662191.

PR 19-OCT-2000; 2000US-0693036.

PR 29-NOV-2000; 2000US-0727344.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;

PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;

XX

DR WPI; 2001-442253/47.

DR P-PSDB; AAM39186.

XX

PT Novel nucleic acids and polypeptides, useful for treating disorders

PT such as central nervous system injuries -

XX

PS Claim 1; SEQ ID NO 545; 10078pp; English.

XX

CC The invention relates to human nucleic acids (AAI57798-AAI61369) and

CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,

CC immunosuppressant and cytostatic activity. The polynucleotides are useful

CC in gene therapy. A composition containing a polypeptide or polynucleotide

CC of the invention may be used to treat diseases of the peripheral nervous

CC system, such as peripheral nervous injuries, peripheral neuropathy and

CC localised neuropathies and central nervous system diseases, such as

CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic

DT 25-MAR-2003 (updated)
 DT 16-APR-1992 (first entry)
 XX
 DE Sequence encoding simian transforming growth factor (TGF) beta-1.
 XX
 KW Hypertension therapy; hypotensive agent; blood pressure modulator;
 KW ss.
 XX
 OS Monkey.
 XX
 FH Key Location/Qualifiers
 FT CDS 262..282
 FT /*tag= a
 FT sig_peptide 283..324
 FT /*tag= b
 FT CDS 325..1098
 FT /*tag= c
 FT mat_peptide 1099..1436
 FT /*tag= d
 XX
 PN WO9119513-A.
 XX
 PD 26-DEC-1991.
 XX
 PF 20-JUN-1991; 91WO-US04449.
 XX
 PR 20-JUN-1990; 90US-0541221.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Oleson FB, Comerreski CR;
 XX
 DR WPI; 1992-024199/03.
 DR P-PSDB; AAR20124.
 XX
 PT Use of transforming growth factor (TGF)-beta and their
 PT antagonists - for modulating blood pressure, for treating
 PT hypertension and hypotension
 XX
 PS Disclosure; Fig 1; 42pp; English.
 XX
 CC A new method for treating hypertension comprises administering a
 CC transforming growth factor (TGF)-beta to an individual at a dose
 CC effective for lowering blood pressure; the TGF-beta may be e.g.
 CC mature TGF-beta, TGF-beta2, a mature TGF-beta1/beta2 hybrid, TGF-
 CC beta1 precursor, a latent TGF-beta2 precursor, hybrid TGF-beta1/TGF-
 CC beta2 precursor, a latent TGF-beta1 complex or a latent TGF-beta2
 CC complex.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 1559 BP; 300 A; 546 C; 446 G; 267 T; 0 other;

 Query Match 71.4%; Score 971.8; DB 13; Length 1559;
 Best Local Similarity 85.1%; Pred. No. 3.2e-187;
 Matches 1146; Conservative 0; Mismatches 142; Indels 59; Gaps 3;

 Qy 11 ATGGCGCCTTCGGGGCTGCGGCTCTTGCCGCTGCTGCTGCCGCTGCTGTGGCTGCTAGTG 70

Db	261	ATGCCGCCCTCCGGGCTGCGGCTGCTGCCGCTGCTGCTACCGCTGCTGTGGCTACTGGTG	320
Qy	71	CTGACGCCTGGCCGGCCGGCCGGCCGACTGTCCACCTGCAAGACCATCGACATGGAGCTG	130
Db	321	CTGACGCCTAGCCGGCCGGCCGAGACTATCCACCTGCAAGACTATCGACATGGAGCTG	380
Qy	131	GTGAAGCGGAAGCGCATCGAGGCCATTTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC	190
Db	381	GTGAAGCGGAAGCGCATCGAGACCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCC	440
Qy	191	AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT	250
Db	441	AGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGCTGCCCGAGGCCGTGCTCGCCCTG	500
Qy	251	TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTGCAACCGGAGCCCGAGCCAGAG	310
Db	501	TACAACAGCACCCGCGACCGGGTGGCCGGGGAGAGTGCAGGAGCCGAGCCCGAACCGGAG	560
Qy	311	GCGGACTACTACGCCAAGGAGGTCAACCGCTGCTAATGGTGGAAAGCGGCAACCAAATC	370
Db	561	GCCGACTACTACGCCAAGGAGGTCAACCGCTGCTAATGGTGGAAACCCACAACGAAATC	620
Qy	371	TATGATAAAATTCAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC	430
Db	621	TATGACAAGTTCAAGCAGAGCACACAGCATATATATGTTCTTCAACACATCAGAGCTC	680
Qy	431	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC	490
Db	681	CGAGAAGCAGTACCTGAACCTGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTC	740
Qy	491	AAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCTGGCGC	550
Db	741	AAGTTAAAAGTCGAGCAGCATGTGGAGCTGTACCAGAAATACAGCAACAATTCTGGCGA	800
Qy	551	TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCTTTGATGTC	610
Db	801	TACCTCAGCAACCGGCTGCTGGCGCCAGCAACTCGCCGGAGTGGTTGTCTTTGATGTC	860
Qy	611	ACCGGAGTTGTGCGGCAGTGGCTGACCCGAGAGAGGCTATAGAGGGTTTTTCGCCTCAGT	670
Db	861	ACCGGAGTTGTGCGGCAGTGGTTGAGCCGCGGAGGGGAAATTGAGGGCTTTTCGCCTTAGC	920
Qy	671	GCCCACTGTTCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT	730
Db	921	GCCCACTGTTCTGTGACAGCAAAGATAACACACTGCAAGTGGACATCAACGGGTTCACT	980
Qy	731	TCTGGCCGCCGGGGTGACCTGGCCACCATTACGGCATGAACCGGCCCTTCTGCTCCTC	790
Db	981	ACCGGCCGCCGAGGTGACCTGGCCACAATTATGGCATGAACCGGCCCTTCTGCTTCTC	1040
Qy	791	ATGGCCACCCCGCTGGAGAGGGCCAGCACCTGCACAGCTCCCGGCACCGCCGAGCCCTG	850
Db	1041	ATGGCCACCCCGCTGGAGAGGGCCCAACATCTGCAAAGCTCCCGGCACCGCCGA-----	1094
Qy	851	GATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCCTGGATACCAAC	910


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Db      1095 -----GCCCTGGACACCAAC 1109
Qy      911 TACTGCTTCAGCTCCACGAGAAGAACTGCTGCGTGCGGCAGCTCTACATTGACTTCCGG 970
      |||
Db      1110 TACTGCTTCAGCTCCACGAGAAGAACTGCTGCGTGCGGCAGCTGTATATTGACTTCCGC 1169
Qy      971 AAGGACCTGGGCTGGAAGTGGATTTCATGAACCCAAGGGCTACCATGCCAATTTCTGCCTG 1030
      |||
Db      1170 AAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCATGCCAACTTCTGCCTG 1229
Qy      1031 GGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCTCTGGCTCTGTAC 1090
      |||
Db      1230 GGGCCCTGTCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAGGTCTCTGGCCCTGTAC 1289
Qy      1091 AACCAGCACAACCCGGGCGCGTCGGCGGCGCCGTGCTGCGTGCCGCAGGCGCTGGAGCCA 1150
      |||
Db      1290 AACCAGCATAACCCGGGCGCCTCGGCGGCGCCGTGCTGCGTGCCGCAGGCGCTGGAGCCA 1349
Qy      1151 CTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATC 1210
      |||
Db      1350 CTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATC 1409
Qy      1211 GTGCGTTCCTGCAAGTGCAAGTGAGGCCCCGCCCCGCCACAGCCCCGCCACCCGGCAG 1270
      |||
Db      1410 GTGCGTTCCTGCAAAATGCAGTGAGGCCCCGCCCCGCCACCCGGCAGGCCGG 1469
Qy      1271 GCGCGGCCACCCCGCCGC-----CTCACCGGGCTGTATTTAAGGACA-TCGTG 1322
      |||
Db      1470 CCGCGGCCACCCCGCCGCTGTCTTGCCCTTGGGGGCTGTATTTAAGGACACCCGTG 1529
Qy      1323 CCCCAAGCCCACTTGGGATCGATTAAA 1349
      |||
Db      1530 CCCCAAGCCACCTGGGGCCCATTA 1556

```

RESULT 12

AAQ13392

ID AAQ13392 standard; DNA; 1821 BP.

XX

AC AAQ13392;

XX

DT 20-NOV-1991 (first entry)

XX

DE Human pro-TGF-beta 1 gene.

XX

KW Osteogenetic; tumoricidal; ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 512..1684

FT /*tag= a

FT sig_peptide 512..598

FT /*tag= b

FT misc_RNA 599..1684

FT /*tag= c

FT /note= "pro-TGF-beta 1"

FT mat_peptide 1346..1684
FT /*tag= e
FT /note= "TGF-beta 1"

XX
PN JP03180192-A.

XX
PD 06-AUG-1991.

XX
PF 07-DEC-1989; 89JP-0318243.

XX
PR 07-DEC-1989; 89JP-0318243.

XX
PA (KIRI) KIRIN BREWERY KK.

XX
DR WPI; 1991-271579/37.

DR P-PSDB; AAR13813.

XX
PT Human pro-TGF-beta 1 prodn., for osteo-genetic activity - by
PT preparing DNA chain contg. base sequence coding for human
PT pre:pro-TGF-beta 1, forming expression vector etc.

XX
PS Claim 1; Fig 1; 16pp; Japanese.

XX
CC The DNA sequence encodes human prepro-TGF-beta 1 which can be
CC produced by recombinant methods, it has osteogenetic and
CC tumoricidal activity.

XX
SQ Sequence 1821 BP; 326 A; 679 C; 508 G; 308 T; 0 other;

Query Match 71.4%; Score 971.4; DB 12; Length 1821;
Best Local Similarity 85.0%; Pred. No. 3.9e-187;
Matches 1135; Conservative 0; Mismatches 141; Indels 59; Gaps 2;

Qy 6 CCGAGATGGCGCCTTCGGGGCTGCGGCTCTTGCCGCTGCTGCTGCCGCTGCTGTGGCTGC 65
|| ||| |||| || ||||||||||| ||||||||||||| ||||||||||||| ||
Db 507 CCCCCATGCCGCCCTCCGGGCTGCGGCTGCTGCGGCTGCTGCTACCGCTGCTGTGGCTAC 566

Qy 66 TAGTGCTGACGCCTGGCCGGCCGGCCCGGACTGTCCACCTGCAAGACCATCGACATGG 125
| ||||||||||||||| ||||||||||| ||||||||||| ||||||||||| ||
Db 567 TGGTGCTGACGCCTGGCCCGCCGGCCCGGGACTATCCACCTGCAAGACTATCGACATGG 626

Qy 126 AGCTGGTGAAGCGGAAGCGCATCGAGGCCATTTCGCGGCCAGATTCTGTCCAAGCTTCGGC 185
||||||||||||||||| ||||||||||| ||||||||||| ||||||||||| ||
Db 627 AGCTGGTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGC 686

Qy 186 TTGCCAGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCGCTGCCTGAGGCAGTACTGG 245
| ||||||||||||||| ||||||||||| ||||||||||| ||||||||||| ||
Db 687 TGGCCAGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCGCTGCCCGAGGCCGTGCTCG 746

Qy 246 CTCTTTACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGC 305
| || ||||||||| ||||||||||| ||||||||||| ||||| |||||||||||||
Db 747 CCCTGTACAACAGCACCCGCGACCGGGTGGCCGGGGAGAGTGCAGAACCGGAGCCCGAGC 806

Qy 306 CAGAGGCGGACTACTACGCCAAGGAGGTCAACCCGCGTGCTAATGGTGGAAGCGGCAACC 365
| ||||| ||||||||||| ||||||||||| ||||||||||| ||||| |||||
Db 807 CTGAGGCCGACTACTACGCCAAGGAGGTCAACCCGCGTGCTAATGGTGGAACCCACAACG 866

Qy	366	AAATCTATGATAAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGG	425
Db	867	AAATCTATGACAAGTTCAAGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAG	926
Qy	426	AGCTCCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGA	485
Db	927	AGCTCCGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGA	986
Qy	486	GGCTCAAGTTAAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCT	545
Db	987	GGCTCAAGTTAAAAAGTGGAGCAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCT	1046
Qy	546	GGCGCTACCTCAGCAACCGGCTGCTGGCCCCAGTGACTCACCGGAGTGGCTGTCTTTG	605
Db	1047	GGCGATACCTCAGCAACCGGCTGCTGGCAACCCAGCGACTCGCCAGAGTGTTATCTTTG	1106
Qy	606	ATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCC	665
Db	1107	ATGTCACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTTCGCC	1166
Qy	666	TCAGTGCCCACTGTTCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGT	725
Db	1167	TTAGCGCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGT	1226
Qy	726	TCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTACCGGCATGAACCGGCCCTTCCTGC	785
Db	1227	TCACTACCGGCCGCCGAGGTGACCTGGCCACCATTATGGCATGAACCGGCCCTTCCTGC	1286
Qy	786	TCCTCATGGCCACCCCGCTGGAGAGGGCCAGCACCTGCACAGCTCCCGGCACCGCCGAG	845
Db	1287	TTCTCATGGCCACCCCGCTGGAGAGGGCCAGCATCTGCAAAGCTCCCGGCACCGCCGA-	1345
Qy	846	CCCTGGATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCCTGGATA	905
Db	1346	-----GCCCTGGACA	1355
Qy	906	CCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTCTACATTGACT	965
Db	1356	CCAACTATTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTGTACATTGACT	1415
Qy	966	TCCGGAAGGACCTGGGCTGGAAGTGGATTATGAACCCAAGGGCTACCATGCCAATTTCT	1025
Db	1416	TCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCAAGGGCTACCATGCCAATTCT	1475
Qy	1026	GCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTC	1085
Db	1476	GCCTCGGGCCCTGCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAGGTCCTGGCCC	1535
Qy	1086	TGTACAACCAGCACAACCCGGGCGCGTCGGCGGCGCCGTGCTGCGTGCCGAGGCGCTGG	1145
Db	1536	TGTACAACCAGCATAACCCGGGCGCCTCGGCGGCGCCGTGCTGCGTGCCGAGGCGCTGG	1595
Qy	1146	AGCCACTGCCCATCGTGTAACGTGGGCGGCAAGCCCAAGGTGGAGCAGCTGTCCAACA	1205
Db	1596	AGCCGCTGCCCATCGTGTAACGTGGGCGGCAAGCCCAAGGTGGAGCAGCTGTCCAACA	1655
Qy	1206	TGATCGTGCGTTCCTGCAAGTGACAGCTGAGGCCCCGCCCCGCCACAGCCCCGCCACCC	1265

[illegible]

RESULT 13

AAN81084

ID AAN81084 standard; cDNA; 1560 BP.

XX

AC AAN81084;

XX

DT 25-MAR-2003 (updated)

DT 09-OCT-1990 (first entry)

XX

DE Coding sequence of simian transforming growth factor-beta 1.

XX

KW Transforming growth factor-beta 1; tumour treatment; ss cDNA.

XX

OS Cercopithecus aethiops.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT	CDS	261..1433
----	-----	-----------

FT /*tag= a

FT	sig peptide	282..323
----	-------------	----------

```
FT                               /*tag=  b
```

```
FT      mat_peptide      1095..1433
```

FT /*tag= c

XX

PN EP293785-A.

XX

PD 07-DEC-1988.

XX

PF 27-MAY-1988; 88EP-0108528.

XX

PR 29-MAY-1987; 87US-0055662.

PR 25-JAN-1988; 88US-0147842.

XX

PA (ONCO) ONCOGEN.

PA (BRIM) BRISTOL-MYERS CO.

XX

PI Purchio AG, Gentry L, Twardzik D;

XX

DR WPI; 1988-347488/49.

DR P-PSDB; AAP80647.

XX

PT Prodn. of simian transforming growth factor beta-1 - by culturing

PT transfected eucaryotic cells, and new precursor proteins, useful for

PT treating tumours.

XX

PS Disclosure; Page ?; pp; English.

XX
 CC The cDNA is prepd. from African green monkey cell line BSC-40 and is
 CC expressed in eukaryotic cells in plasmid pSV2. There is 100% homology
 CC between mature simian and human TGF-beta 1. The plasmid also contains
 CC the SV40 promoter and a selection marker, esp. DHFR.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 1560 BP; 301 A; 547 C; 445 G; 267 T; 0 other;

Query Match 71.3%; Score 970.8; DB 9; Length 1560;
 Best Local Similarity 85.0%; Pred. No. 5.1e-187;
 Matches 1146; Conservative 0; Mismatches 142; Indels 60; Gaps 3;

Qy	11	ATGGCGCCTTCGGGGCTGCGGCTCTTGCCGCTGCTGCTGCCGCTGCTGTGGCTGCTAGTG	70
Db	261	ATGCCGCCCTCCGGGCTGCGGCTGCTGCCGCTGCTGCTACCGCTGCTGTGGCTACTGGTG	320
Qy	71	CTGACGCCTGGCCGGCCGGCCGCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG	130
Db	321	CTGACGCCTAGCCGGCCGGCCGAGACTATCCACCTGCAAGACTATCGACATCGAGCTG	380
Qy	131	GTGAAGCGGAAGCGCATCGAGGCCATTGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC	190
Db	381	GTGAAGCGGAAGCGCATCGAGACCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCC	440
Qy	191	AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT	250
Db	441	AGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGCTGCCCGAGGCCGTGCTCGCCCTG	500
Qy	251	TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTGCAACCGGAGCCCGAGCCAGAG	310
Db	501	TACAACAGCACCCGCGACCGGGTGGCCGGGGAGAGTGCAGGAGCCCGAGCCCGAACCGGAG	560
Qy	311	GCGGACTACTACGCCAAGGAGGTCAACCGCGTGCTAATGGTGGAAAGCGGCAACCAAATC	370
Db	561	GCCGACTACTACGCCAAGGAGGTCAACCGCGTGCTAATGGTGGAAACCCACAACGAAATC	620
Qy	371	TATGATAAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC	430
Db	621	TATGACAAGTTCAAGCAGAGCACACAGCATATATATGTTCTTCAACACATCAGAGCTC	680
Qy	431	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC	490
Db	681	CGAGAAGCAGTACCTGAACCTGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTC	740
Qy	491	AAGTTAAAAGTGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCTGGCGC	550
Db	741	AAGTTAAAAGTCGAGCAGCATGTGGAGCTGTACCAGAAATACAGCAACAATTCTGGCGA	800
Qy	551	TACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCTTTGATGTC	610
Db	801	TACCTCAGCAACCGGCTGCTGGCGCCAGCAACTCGCCGGAGTGGTTGTCTTTGATGTC	860
Qy	611	ACCGGAGTTGTGCGGCAGTGGCTGACCCGAGAGAGGCTATAGAGGGTTTTCGCCTCAGT	670
Db	861	ACCGGAGTTGTGCGGCAGTGGTTGAGCCGCGGAGGGGAAATTGAGGGCTTTCGCCTTAGC	920

QY	671	GCCCACTGTTCTTCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT	730
Db	921	GCCCACTGCTCCTGTGACAGCAAAGATAACACACTGCAAGTGGACATCAACGGGTTCACT	980
QY	731	TCTGGCCGCGCGGGGTGACCTGGCCACCATTACGGCATGAACCGGCCCTTCCTGCTCCTC	790
Db	981	ACCGGCCGCGCGAGGTGACCTGGCCACAATTATGCGCATGAACCGGCCCTTCCTGCTTCTC	1040
QY	791	ATGGCCACCCCGCTGGAGAGGGCCAGCACCTGCACAGCTCCCGGCACCGCCGAGCCCTG	850
Db	1041	ATGGCCACCCCGCTGGAGAGGGCCCAACATCTGCAAAGCTCCCGGCACCGCCGAG-----	1095
QY	851	GATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCCTGGATACCAAC	910
Db	1096	-----CCCTGGACACCAAC	1109
QY	911	TACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTCTACATTGACTTCCGG	970
Db	1110	TACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTGTATATTGACTTCCGC	1169
QY	971	AAGGACCTGGGCTGGAAGTGGATTATGAACCCAAGGGCTACCATGCCAATTTCTGCCTG	1030
Db	1170	AAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCATGCCAACTTCTGCCTG	1229
QY	1031	GGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCTTGGCTCTGTAC	1090
Db	1230	GGGCCCTGTCCCTACATTGAGCCTGGACACGCAGTACAGCAAGGTCTTGGCCCTGTAC	1289
QY	1091	AACCAGCACAACCCGGGCGCTCGGCGGCGCCGTGCTGCGTGCCGCAGGCGCTGGAGCCA	1150
Db	1290	AACCAGCATAACCCGGGCGCCTCGGCGGCGCCGTGCTGCGTGCCGCAGGCGCTGGAGCCA	1349
QY	1151	CTGCCCATCGTGTAATACTGAGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATC	1210
Db	1350	CTGCCCATCGTGTAATACTGAGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATC	1409
QY	1211	GTGCGTTCTTGCAAGTGCAGCTGAGGCCCGCCCCGCCACAGCCCCGCCACCCGGCAG	1270
Db	1410	GTGCGCTCCTGAAAATGCAGCTGAGGCCCGCCCCGCCCGCCCCACCCGGCAGGCCCG	1469
QY	1271	GCCCCGCCCCACCCCGCCCGCCT-----CACCGGGGCTGTATTTAAGGACA-TCGT	1321
Db	1470	GCCCCGCCCCACCCACCCCGCTGTCTTGCCCTTGGGGGCTGTATTTAAGGACACCCGT	1529
QY	1322	GCCCCAAGCCCACTTGGGATCGATTAAA	1349
Db	1530	GCCCCAAGCCCACTGGGGCCCCATTAA	1557

DT 09-JAN-2003 (updated)
 DT 14-AUG-1990 (first entry)
 XX
 DE Simian Transforming growth factor - Beta1.
 XX
 KW HIV; AIDS; SIV; vaccine; AZT; CD4; cytokines; growth
 KW factors; ds.
 XX
 OS Cebus apella.
 XX
 FH Key Location/Qualifiers
 FT CDS 267..1437
 FT /*tag= a
 FT mat_peptide 1103..1437
 FT /*tag= b
 XX
 PN EP356935-A.
 XX
 PD 07-MAR-1990.
 XX
 PF 25-AUG-1989; 89EP-0115719.
 XX
 PR 25-AUG-1988; 88US-0236698.
 XX
 PA (ONCO) ONCOGEN LP.
 XX
 PI Brankovan V, Lioubin M, Purchio A;
 XX
 DR WPI; 1990-068723/10.
 DR P-PSDB; AAR05663.
 XX
 PT Compsns. contg. transforming growth factor beta -
 PT used for inhibitions of HIV infection and replication in vivo.
 XX
 PS Disclosure; Fig 1; 20pp; English.
 XX
 CC TGF-beta may be used in vivo to prevent formation of syncytia and
 CC inhibit HIV infection. TGF may also be used with other HIV treatments
 CC (AZT, soluble CD4 etc.).
 CC (Updated on 09-JAN-2003 to add missing OS field.)
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 1560 BP; 301 A; 547 C; 445 G; 267 T; 0 other;

 Query Match 71.3%; Score 970.8; DB 11; Length 1560;
 Best Local Similarity 85.0%; Pred. No. 5.1e-187;
 Matches 1146; Conservative 0; Mismatches 142; Indels 60; Gaps 3;

 Qy 11 ATGGCGCCTTCGGGGCTGCGGCTCTTGCCGCTGCTGCTGCCGCTGCTGTGGCTGCTAGTG 70
 ||| |||| || ||||||||| ||||||||||| ||||||||||| || |||
 Db 261 ATGCCGCCCTCCGGGCTGCGGCTGCTGCCGCTGCTGCTACCGCTGCTGTGGCTACTGGTG 320

 Qy 71 CTGACGCCTGGCCGGCCGGCCGGCCGACTGTCCACCTGCAAGACCATCGACATGGAGCTG 130
 ||||||||| ||||||||||| ||||| ||||||||||| ||||||||| |||||
 Db 321 CTGACGCCTAGCCGGCCGGCCGAGGACTATCCACCTGCAAGACTATCGACATCGAGCTG 380

 Qy 131 GTGAAGCGGAAGCGCATCGAGGCCATTGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC 190

Db	381	 GTGAAGCGGAAGCGCATCGAGACCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCC	440
Qy	191	AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTT	250
Db	441	 AGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGCTGCCCGAGGCCGTGCTCGCCCTG	500
Qy	251	TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTGGAACCGGAGCCCGAGCCAGAG	310
Db	501	 TACAACAGCACCCGCGACCGGGTGGCCGGGGAGAGTGCGGAGCCGAGCCCGAACCGGAG	560
Qy	311	GCGGACTACTACGCCAAGGAGGTCAACCGCGTGCTAATGGTGGAAGCGGCAACCAAATC	370
Db	561	 GCCGACTACTACGCCAAGGAGGTCAACCGCGTGCTAATGGTGGAACCCACAACGAAATC	620
Qy	371	TATGATAAAATTCAAGGGCACCCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC	430
Db	621	 TATGACAAGTTCAAGCAGAGCACACAGCATATATATGTTCTTCAACACATCAGAGCTC	680
Qy	431	CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTC	490
Db	681	 CGAGAAGCAGTACCTGAACCTGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTC	740
Qy	491	AAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGGCGC	550
Db	741	 AAGTTAAAAGTCGAGCAGCATGTGGAGCTGTACCAGAAATACAGCAACAATTCTGGCGA	800
Qy	551	TACCTCAGCAACCGGCTGCTGGCCCCCAGTGAAGTCAACCGGAGTGGCTGTCTTTGATGTC	610
Db	801	 TACCTCAGCAACCGGCTGCTGGCGCCAGCAACTCGCCGGAGTGGTTGTCTTTGATGTC	860
Qy	611	ACCGGAGTTGTGCGGCAGTGGCTGACCCGAGAGAGGCTATAGAGGGTTTTTCGCTCAGT	670
Db	861	 ACCGGAGTTGTGCGGCAGTGGTTGAGCCGCGGAGGGGAAATTGAGGGCTTTTCGCTTAGC	920
Qy	671	GCCCACTGTTCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAAT	730
Db	921	 GCCCACTGCTCCTGTGACAGCAAAGATAACACACTGCAAGTGACATCAACGGGTTCACT	980
Qy	731	TCTGGCCGCCGGGGTGACCTGGCCACCATTACGGCATGAACCGGCCCTTCTGCTCCTC	790
Db	981	 ACCGGCCGCCGAGGTGACCTGGCCACAATTCATGGCATGAACCGGCCCTTCTGCTTCTC	1040
Qy	791	ATGGCCACCCCGCTGGAGAGGGGCCAGCACCTGCACAGCTCCCGGCACCGCCGAGCCCTG	850
Db	1041	 ATGGCCACCCCGCTGGAGAGGGGCCAACATCTGCAAAGCTCCCGGCACCGCCGAG-----	1095
Qy	851	GATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCCTGGATACCAAC	910
Db	1096	----- -----CCCTGGACACCAAC	1109
Qy	911	TACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTCTACATTGACTTCCGG	970
Db	1110	 TACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTGTATATTGACTTCCGC	1169
Qy	971	AAGGACCTGGGCTGGAAGTGGATTTCATGAACCCAAAGGGCTACCATGCCAATTTCTGCCTG	1030


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Db      1170 AAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCATGCCAACTTCTGCCTG 1229
Qy      1031 GGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCTGGCTCTGTAC 1090
        |||
Db      1230 GGGCCCTGTCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAGGTCTGGCCCTGTAC 1289
Qy      1091 AACCAGCAACAACCCGGGCGCGTCGGCGGCGCCGTGCTGCGTGCCGCAGGCGCTGGAGCCA 1150
        |||
Db      1290 AACCAGCATAACCCGGGCGCCTCGGCGGCGCCGTGCTGCGTGCCGCAGGCGCTGGAGCCA 1349
Qy      1151 CTGCCCATCGTGTACTACGTGGGCGCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATC 1210
        |||
Db      1350 CTGCCCATCGTGTACTACGTGGGCGCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATC 1409
Qy      1211 GTGCGTTCCTGCAAGTGCAAGTGGAGGCCCCGCCCCGCCCCACAGCCCCGCCCCACCCGGCAG 1270
        |||
Db      1410 GTGCGTTCCTGAAAAATGCAGCTGAGGCCCCGCCCCGCCCCACCCCGGCAGGCCCG 1469
Qy      1271 GCCCCGCCCCACCCCGCCCGCCT-----CACCGGGGCTGTATTTAAGGACA-TCGT 1321
        |||
Db      1470 GCCCCGCCCCACCCCGCCCGCTGTCTTGCCCTTGGGGGCTGTATTTAAGGACACCCGT 1529
Qy      1322 GCCCCAAGCCCACTTGGGATCGATTAAA 1349
        |||
Db      1530 GCCCCAAGCCCACCTGGGGCCCCATTAA 1557

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RESULT 15

AAT05876

ID AAT05876 standard; cDNA; 2745 BP.

XX

AC AAT05876;

XX

DT 25-JUN-1996 (first entry)

XX

DE cDNA encoding transforming growth factor-beta 1.

XX

KW macrophage inducible nitric oxide synthase; iNOS; constitutive NOS;

KW interleukin-1-beta; transforming growth factor-beta; TGF-beta; IL1-beta;

KW nitric oxide production; hypotension; inflammation; septic shock;

KW treatment; ds.

XX

OS Mammalian sp.

XX

FH Key Location/Qualifiers

FT CDS 842..2017

FT /*tag= a

FT /product= transforming growth factor-beta 1

XX

PN WO9526745-A1.

XX

PD 12-OCT-1995.

XX

PF 05-APR-1994; 94WO-US03705.

XX

PR 05-APR-1994; 94WO-US03705.

XX

PA (HARD) HARVARD COLLEGE.
 XX
 PI Lee M, Perrella MA;
 XX
 DR WPI; 1995-358443/46.
 DR P-PSDB; AAR83054.
 XX
 PT Treatment of hypotension, esp. in septic shock - by administering
 PT transforming growth factor-beta e.g. to inhibit inducible nitric
 PT oxide synthase gene transcription
 XX
 PS Disclosure; Fig 15; 52pp; English.
 XX
 CC The cDNA encodes transforming growth factor-beta 1 (TGF-beta 1) which
 CC has been found to inhibit inducible nitric oxide synthase (iNOS) gene
 CC transcription, esp. in interleukin-1-beta (IL1-beta) stimulated rat
 CC smooth muscle cells, and at a dose which does not inhibit constitutive
 CC NOS. TGF-beta 1 or 2 (AAR83055) or their active fragments, can be used
 CC in the treatment of hypotension, such as that associated with severe
 CC inflammation or septic shock.
 XX
 SQ Sequence 2745 BP; 527 A; 938 C; 801 G; 479 T; 0 other;

Query Match 71.2%; Score 969; DB 16; Length 2745;
 Best Local Similarity 84.7%; Pred. No. 1.3e-186;
 Matches 1148; Conservative 0; Mismatches 145; Indels 62; Gaps 3;

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Qy      6 CCGAGATGGCGCCTTCGGGGCTGCGGCTCTTGCCGCTGCTGCTGCCGCTGCTGTGGCTGC 65
      ||  ||| |||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    837 CCCCCATGCCGCCCTCCGGGCTGCGGCTGCTGCCGCTGCTGCTACCGCTGCTGTGGCTAC 896

Qy      66 TAGTGCTGACGCCTGGCCGGCCGGCCGGGACTGTCCACCTGCAAGACCATCGACATGG 125
      | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    897 TGGTGCTGACGCCTGGCCCGCCGGCCGGGACTATCCACCTGCAAGACTATCGACATGG 956

Qy     126 AGCTGGTGAAGCGGAAGCGCATCGAGGCCATTTCGCGGCCAGATTCTGTCCAAGCTTCGGC 185
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    957 AGCTGGTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGC 1016

Qy     186 TTGCCAGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCGCTGCCTGAGGCAGTACTGG 245
      | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1017 TCGCCAGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCGCTGCCCGAGGCCGTGCTCG 1076

Qy     246 CTCTTTACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTGCAACCGGAGCCCGAGC 305
      | || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1077 CCCTGTACAACAGCACCCGCGACCGGGTGGCCGGGGAGAGTGCAGAACCGGAGCCCGAGC 1136

Qy     306 CAGAGGCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGAAAGCGGCAACC 365
      | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1137 CTGAGGCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGAAACCCACAACG 1196

Qy     366 AAATCTATGATAAAATTCAGGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGG 425
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1197 AAATCTATGACAAGTTCAAGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAG 1256

Qy     426 AGCTCCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCT-- 483
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db	1257	AGCTCCGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGA	1316
Qy	484	-GAGGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATT	542
Db	1317	GGAGGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTGTACCAGAAATACAGCAACAATT	1376
Qy	543	CCTGGCGCTACCTCAGCAACCGGCTGCTGGCCCCAGTGACTACCCGGAGTGGCTGTCTCT	602
Db	1377	CCTGGCGATACCTCAGCAACCGGCTGCTGGCACCAGCGACTCGCCAGAGTGGTTATCTT	1436
Qy	603	TTGATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTC	662
Db	1437	TTGATGTCACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTC	1496
Qy	663	GCCTCAGTGCCCACTGTTCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACG	722
Db	1497	GCCTTAGCGCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACG	1556
Qy	723	GGTTCAATTCTGGCCGCCGGGTGACCTGGCCACCATTACGGCATGAACCGGCCCTTTC	782
Db	1557	GGTTCACTACCGGCCGCCGAGGTGACCTGGCCACCATTATGGCATGAACCGGCCCTTTC	1616
Qy	783	TGCTCCTCATGGCCACCCCGCTGGAGAGGGCCAGCACCTGCACAGCTCCCGGCACCGCC	842
Db	1617	TGCTTCTCATGGCCACCCCGCTGGAGAGGGCCAGCATCTGCAAAGCTCCCGGCACCGCC	1676
Qy	843	GAGCCCTGGATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCCTGG	902
Db	1677	GA-----GCCCTGG	1685
Qy	903	ATACCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTCTACATTG	962
Db	1686	ACACCAACTATTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTGTACATTG	1745
Qy	963	ACTTCCGGAAGGACCTGGGCTGGAAGTGGATTATGAACCCAAGGGCTACCATGCCAATT	1022
Db	1746	ACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCAGAGCCCAAGGGCTACCATGCCAATT	1805
Qy	1023	TCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCTCTGG	1082
Db	1806	TCTGCCTCGGGCCCTGCCCCATACATTGGAGCCTGGACACGCAGTACAGCAAGGTCTCTGG	1865
Qy	1083	CTCTGTACAACCAGCACAAACCGGGCGCGTGGCGGGCGCCGTGCTGCGTGCCGCAGGCGC	1142
Db	1866	CCCTGTACAACCAGCATAAACCGGGCGCCTCGGCGGGCGCCGTGCTGCGTGCCGCAGGCGC	1925
Qy	1143	TGGAGCCACTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCA	1202
Db	1926	TGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGCAAGCCCAAGGTGGAGCAGCTGTCCA	1985
Qy	1203	ACATGATCGTGCGTTCTGCAAGTGCAGCTGAGGCCCGCCCCGCCCCACAGCCCCGCCCA	1262
Db	1986	ACATGATCGTGCGTCTCTGCAAGTGCAGCTGAGGTCCCGCCCCGCCCCGCCCCGCCCGG	2045
Qy	1263	CCCGGCAGGCCCGGCCCAACCCCGCCCGCCT-----CACCGGGCTGTATTTAAGG	1314
Db	2046	CAGGCCCGGCCCAACCCCGCCCGCCTGCTGCTGCCCCATGGGGCTGTATTTAAGG	2105

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Qy      1315 ACATCGTGCCCCAAGCCCACTTGGGATCGATTAAA 1349
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Db      2106 ACACCGTGCCCCAAGCCCACTTGGGGCCCCATTAA 2140

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Search completed: October 27, 2003, 19:11:34
Job time : 419.887 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 18:35:27 ; Search time 404.529 Seconds
(without alignments)
9022.658 Million cell updates/sec

Title: US-10-017-372E-38
Perfect score: 1361
Sequence: 1 tggtagcgagatggcgccctt.....cgattaaagcgccgcgact 1361

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1792395 seqs, 1340900451 residues

Total number of hits satisfying chosen parameters: 3584790

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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- 17: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
	1	973	71.5	1821	14	US-10-087-268-1	Sequence 1, Appli
	2	972.6	71.5	2742	14	US-10-037-270-220	Sequence 220, Appl
	3	971.4	71.4	1821	14	US-10-087-268-4	Sequence 4, Appli
	4	969	71.2	2745	11	US-09-948-002-28	Sequence 28, Appl
	5	850.2	62.5	2094	11	US-09-948-002-1	Sequence 1, Appli
	6	830.6	61.0	1585	11	US-09-948-002-27	Sequence 27, Appl
	7	657.2	48.3	1376	10	US-09-756-283A-19	Sequence 19, Appl
	8	594.6	43.7	1352	10	US-09-756-283A-21	Sequence 21, Appl
	9	354.4	26.0	489	11	US-09-911-904-167	Sequence 167, App
	10	308.6	22.7	339	10	US-09-813-271B-1	Sequence 1, Appli
	11	249	18.3	2574	11	US-09-906-158-3	Sequence 3, Appli
	12	249	18.3	2574	13	US-10-028-158-20	Sequence 20, Appl
	13	242.8	17.8	4382	12	US-09-957-458B-9	Sequence 9, Appli
	14	239.6	17.6	2879	11	US-09-906-158-10	Sequence 10, Appl
	15	227.2	16.7	336	10	US-09-813-271B-7	Sequence 7, Appli
	16	209.4	15.4	339	10	US-09-813-271B-5	Sequence 5, Appli
c	17	185.4	13.6	2381	12	US-10-311-455-2384	Sequence 2384, Ap
	18	183	13.4	4267	11	US-09-948-002-47	Sequence 47, Appl
	19	182.4	13.4	336	10	US-09-813-271B-11	Sequence 11, Appl
	20	181.2	13.3	2381	12	US-10-311-455-2383	Sequence 2383, Ap
	21	180.8	13.3	336	10	US-09-813-271B-9	Sequence 9, Appli
	22	158.2	11.6	339	10	US-09-813-271B-3	Sequence 3, Appli
	23	158.2	11.6	2570	12	US-09-960-706-663	Sequence 663, App
	24	158.2	11.6	2912	13	US-10-044-090-323	Sequence 323, App
c	25	141.6	10.4	597	9	US-09-864-761-15319	Sequence 15319, A
c	26	134.8	9.9	154	9	US-09-864-761-31841	Sequence 31841, A
c	27	131.8	9.7	206	10	US-09-833-381-577	Sequence 577, App
c	28	122	9.0	537	9	US-09-864-761-8844	Sequence 8844, Ap
c	29	121	8.9	148	9	US-09-864-761-25510	Sequence 25510, A
	30	117	8.6	181	10	US-09-833-381-1416	Sequence 1416, Ap
	31	104.8	7.7	851	13	US-10-027-632-152938	Sequence 152938,
	32	102.2	7.5	29000	11	US-09-906-158-17	Sequence 17, Appl
c	33	100.4	7.4	224	10	US-09-833-381-73	Sequence 73, Appl
	34	79.4	5.8	450	11	US-09-918-995-6145	Sequence 6145, Ap
c	35	69.8	5.1	431	9	US-09-864-761-18644	Sequence 18644, A
c	36	69.4	5.1	176	10	US-09-833-381-571	Sequence 571, App
	37	69	5.1	584	12	US-10-029-386-9758	Sequence 9758, Ap
	38	68.2	5.0	176	12	US-10-029-386-23458	Sequence 23458, A
c	39	64	4.7	363	10	US-09-833-381-585	Sequence 585, App
	40	62.6	4.6	364	12	US-10-029-386-26476	Sequence 26476, A
	41	62.6	4.6	544	12	US-10-029-386-12776	Sequence 12776, A
	42	62.6	4.6	927	12	US-10-244-718-1	Sequence 1, Appli
	43	57.4	4.2	486	11	US-09-918-995-25641	Sequence 25641, A
	44	55.2	4.1	594	13	US-10-027-632-141376	Sequence 141376,
	45	50.4	3.7	658	9	US-09-765-527-254	Sequence 254, App

ALIGNMENTS

US-10-087-268-1

; Publication No. US20030119010A1

; APPLICANT: Jonsonn, Julie Ruth

; TITLE OF INVENTION: Polypeptides and polynucleotides linked to a disease or condition

; CURRENT APPLICATION NUMBER: US/10/087,268

; NUMBER OF SEQ ID NOS: 6

; SEQ ID NO 1

; TYPE: DNA

; FEATURE:

; LOCATION: (1) .. (511)

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; NAME/KEY: CDS
; LOCATION: (512)..(1684)
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; NAME/KEY: sig peptide
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; OTHER INFORMATION:

; LOCATION: (1685)..(1821)

US-10-087-268-1

Best Local Similarity 85.1%; Pred. No. 1.4e-254;

Matches 1136; Conservative 0; Mismatches 140; Indels 59; Gaps 2;

Db 507 CCCCCATGCCGCCCTCCGGGCTGCGGGCTGCTGCCGCTGCTGCTACCGCTGCTGTGGCTAC 566

Db 567 TGGTGCTGACGCCTGGCCGGCCGGCCGCGGGACTATCCACCTGCAAGACTATCGACATGG 626

Db 627 AGCTGGTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGC 686

Db 687 TCGCCAGCCCCCGAGCCAGGGGGAGGTGCCGCCGGCCCGCTGCCCGAGGCCGTGCTCG 746

Db 747 CCCTGTACAACAGCACCCGCGACCGGGTGGCCGGGGAGAGTGCAGAACCGGAGCCCGAGC 806

Qy	306	CAGAGGCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAGCGGCAACC	365
Db	807	CTGAGGCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAACCCACAACG	866
Qy	366	AAATCTATGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGG	425
Db	867	AAATCTATGACAAGTTCAAGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAG	926
Qy	426	AGCTCCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGA	485
Db	927	AGCTCCGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGCAGAGCTGCGTCTGCTGA	986
Qy	486	GGCTCAAGTTAAAAGTGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCT	545
Db	987	GGCTCAAGTTAAAAGTGAGCAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCT	1046
Qy	546	GGCGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGCGTCTCTTTG	605
Db	1047	GGCGATACTCAGCAACCGGCTGCTGGCACCAGCGACTCGCCAGAGTGCGTTATCTTTTG	1106
Qy	606	ATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTCGCC	665
Db	1107	ATGTCACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTTCGCC	1166
Qy	666	TCAGTGCCCACTGTTCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGT	725
Db	1167	TTAGCGCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGACATCAACGGGT	1226
Qy	726	TCAATTCTGGCCGCCGGGTGACCTGGCCACCATTACGGGCATGAACCGGCCCTTCTGC	785
Db	1227	TCACTACCGGCCGCCGAGGTGACCTGGCCACCATTATGGCATGAACCGGCCCTTCTGC	1286
Qy	786	TCCTCATGGCCACCCGCTGGAGAGGGCCAGCACCTGCACAGCTCCCGGCACCGCCGAG	845
Db	1287	TTCTCATGGCCACCCGCTGGAGAGGGCCAGCATCTGCAAAGCTCCCGGCACCGCCGA-	1345
Qy	846	CCCTGGATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCCTGGATA	905
Db	1346	-----GCCCTGGACA	1355
Qy	906	CCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTCTACATTGACT	965
Db	1356	CCAACTATTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTGTACATTGACT	1415
Qy	966	TCCGGAAGGACCTGGGCTGGAAGTGGATTTCATGAACCAAGGGCTACCATGCCAATTTCT	1025
Db	1416	TCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCATGCCAATTCT	1475
Qy	1026	GCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTC	1085
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[illegible]

RESULT 2

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; Sequence 220, Application US/10037270
; Publication No. US20030104529A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: Tillinghast, John
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20030104529A1el Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/10/037,270
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1104
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 220
; LENGTH: 2742
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (842)..(2014)

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US-10-037-270-220

Query Match 71.5%; Score 972.6; DB 14; Length 2742;
Best Local Similarity 84.9%; Pred. No. 2e-254;
Matches 1149; Conservative 0; Mismatches 144; Indels 60; Gaps 3;

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Qy     66 TAGTGCTGACGCCTGGCCGGCCGGCCGGCCGACTGTCCACCTGCAAGACCATCGACATGG 125
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Db    897 TGGTGCTGACGCCTGGCCGGCCGGCCGGCCGACTATCCACCTGCAAGACTATCGACATGG 956

Qy    126 AGCTGGTGAAGCGGAAGCGCATCGAGGCCATTTCGCGGCCAGATTCTGTCCAAGCTTCGGC 185
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    957 AGCTGGTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGC 1016

Qy    186 TTGCCAGCCCCCGAGCCAGGGGACGTGCCGCCCGGCCGCTGCCTGAGGCAGTACTGG 245
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Db   1017 TCGCCAGCCCCCGAGCCAGGGGAGGTGCCGCCCGGCCGCTGCCCAGGCCGTGCTCG 1076

Qy    246 CTCTTTACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGC 305
      | || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   1077 CCCTGTACAACAGCACCCGCGACCGGGTGGCCGGGGAGAGTGCAGAACCGGAGCCCGAGC 1136

Qy    306 CAGAGGCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAGCGGCAACC 365
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Db   1137 CTGAGGCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAACCCACAACG 1196

Qy    366 AAATCTATGATAAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGG 425
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Db   1317 GGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCT 1376

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Db   1377 GGCGATACCTCAGCAACCGGTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTG 1436

Qy    606 ATGTCACCGGAGTTGTGCGGCAGTGCTGACCCGAGAGAGGCTATAGAGGGTTTTCGCC 665
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[illegible]

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;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: 5'UTR
;   LOCATION: (1)..(511)
;   OTHER INFORMATION:
;   NAME/KEY: CDS
;   LOCATION: (512)..(1684)
;   OTHER INFORMATION:
;   NAME/KEY: sig_peptide
;   LOCATION: (512)..(598)
;   OTHER INFORMATION:
;   NAME/KEY: 3'UTR
;   LOCATION: (1685)..(1821)
;   OTHER INFORMATION:
US-10-087-268-4

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Query Match          71.4%;   Score 971.4;   DB 14;   Length 1821;
Best Local Similarity 85.0%;   Pred. No. 3.9e-254;
Matches 1135;   Conservative    0;   Mismatches 141;   Indels    59;   Gaps      2;

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Qy      6 CCGAGATGGCGCCTTCGGGGCTGCGGCTCTTGCCGCTGCTGCTGCCGCTGCTGTGGCTGC 65
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Db      567 TGGTGCTGACGCCTGGCCCCGCCGGCCGGGACTATCCACCTGCAAGACTATCGACATGG 626

Qy      126 AGCTGGTGAAGCGGAAGCGCATCGAGGCCATTCCGCGGCCAGATTCTGTCCAAGCTTCGGC 185
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Db      627 AGCTGGTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGC 686

Qy      186 TTGCCAGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGG 245
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Db      687 TCGCCAGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGCTGCCCCAGGCCGTGCTCG 746

Qy      246 CTCTTTACAACAGTACCCGCGACCGGGTAGCCGGGGAAAAGTGTGCAACCGGAGCCCGAGC 305
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Db      747 CCCTGTACAACAGCACCCGCGACCGGGTGGCCGGGGAGAGTGCAGAACCGGAGCCCGAGC 806

Qy      306 CAGAGGCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAGCGGCAACC 365
      | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      807 CTGAGGCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAACCCACAACG 866

Qy      366 AAATCTATGATAAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGG 425
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Db      927 AGCTCCGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGA 986

Qy      486 GGCTCAAGTTAAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCT 545
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Db      987 GGCTCAAGTTAAAAAGTGGAGCAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCT 1046

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Qy 546 GGCCTACCTCAGCAACCGGCTGCTGGCCCCAGTGACTCACCGGAGTGGCTGTCTTTG 605
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 Db 1047 GGCCTACCTCAGCAACCGGCTGCTGGCACCAGCGACTCGCCAGAGTGGTTATCTTTG 1106
 Qy 606 ATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGAGAGAGGCTATAGAGGGTTTTCGCC 665
 |||||
 Db 1107 ATGTCACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTTCGCC 1166
 Qy 666 TCAGTGCCCACTGTTCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGT 725
 || |||||
 Db 1167 TTAGCGCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGT 1226
 Qy 726 TCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTACGGCATGAACCGGCCCTTCTGC 785
 ||| |||||
 Db 1227 TCACTACCGCCGCCGAGGTGACCTGGCCACCATTATGGCATGAACCGGCCTTTCTGC 1286
 Qy 786 TCCTCATGGCCACCCGCTGGAGAGGGCCAGCACCTGCACAGCTCCCGGCACCGCCGAG 845
 |||||
 Db 1287 TTCTCATGGCCACCCGCTGGAGAGGGCCAGCATCTGCAAAGCTCCCGGCACCGCCGA- 1345
 Qy 846 CCCTGGATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCCTGGATA 905
 |||||
 Db 1346 -----GCCCTGGACA 1355
 Qy 906 CCAACTACTGCTTCAGCTCCACGAGAAGAACTGCTGCGTGCGGCAGCTCTACATTGACT 965
 |||||
 Db 1356 CCAACTATTGCTTCAGCTCCACGAGAAGAACTGCTGCGTGCGGCAGCTGTACATTGACT 1415
 Qy 966 TCCGGAAGGACCTGGGCTGGAAGTGGAATTCATGAACCCAAGGGCTACCATGCCAATTTCT 1025
 |||||
 Db 1416 TCCGCAAGGACCTCGGCTGGAAGTGGAATCCACGAGCCCAAGGGCTACCATGCCAATTCT 1475
 Qy 1026 GCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTC 1085
 |||||
 Db 1476 GCCTCGGGCCCTGCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAGGTCCTGGCCC 1535
 Qy 1086 TGTACAACCAGCACAAACCGGGCGCGTCCGGCGCGCGTGTGCGTGCCGAGGCGCTGG 1145
 |||||
 Db 1536 TGTACAACCAGCATAACCGGGCGCCTCGGCGGGCGCGTGTGCGTGCCGAGGCGCTGG 1595
 Qy 1146 AGCCACTGCCCATCGTGTAACGTGGGCGCAAGCCCAAGGTGGAGCAGCTGTCCAACA 1205
 |||||
 Db 1596 AGCCGCTGCCCATCGTGTAACGTGGGCGCAAGCCCAAGGTGGAGCAGCTGTCCAACA 1655
 Qy 1206 TGATCGTGCGTTCCTGCAAGTGACAGCTGAGGCCCCGCCCCGCCCCAGCCCCGCCCCACC 1265
 |||||
 Db 1656 TGATCGTGCGTTCCTGCAAGTGACAGCTGAGGTCCCCGCCCCGCCCCGCCCCGCCCCGCGAG 1715
 Qy 1266 GGCAGGCCCCGCCCCACCCCGCCCCGCT- - - - -CACCGGGGCTGTATTTAAGGACA 1317
 |||||
 Db 1716 GCCCGGCCCCACCCCGCCCCGCCCCGCTGCTTGCCCATGGGGGCTGTATTTAAGGACA 1775
 Qy 1318 TCGTGCCCCAAGCCC 1332
 |||||
 Db 1776 CCGTGCCCCAAGCC 1790

US-09-948-002-28

US-09-948-002-28

Matches 1148; Conservative 0; Mismatches 145; Indels 62; Gaps 3;

[illegible]

Db	1197	AAATCTATGACAAGTTC AAGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAG	1256
Qy	426	AGCTCCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCT--	483
Db	1257	AGCTCCGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGA	1316
Qy	484	-GAGGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATT	542
Db	1317	GGAGGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTGTACCAGAAATACAGCAACAATT	1376
Qy	543	CCTGGCGCTACCTCAGCAACCGGTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCTT	602
Db	1377	CCTGGCGATACCTCAGCAACCGGTGCTGGCACCAGCGACTCGCCAGAGTGGTTATCTT	1436
Qy	603	TTGATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTC	662
Db	1437	TTGATGTCACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTC	1496
Qy	663	GCCTCAGTGCCCACTGTTCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACG	722
Db	1497	GCCTTAGCGCCCACTGTTCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACG	1556
Qy	723	GGTTCAATTCTGGCCGCCGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCC	782
Db	1557	GGTTCACTACCGGCCGCCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCCTTCC	1616
Qy	783	TGCTCCTCATGGCCACCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCC	842
Db	1617	TGCTTCTCATGGCCACCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGCC	1676
Qy	843	GAGCCCTGGATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCCTGG	902
Db	1677	GA-----GCCCTGG	1685
Qy	903	ATACCAACTACTGCTTCAGCTCCACGAGAAGAACTGCTGCGTGCGGCAGCTCTACATTG	962
Db	1686	ACACCAACTATTGCTTCAGCTCCACGAGAAGAACTGCTGCGTGCGGCAGCTGTACATTG	1745
Qy	963	ACTTCCGGAAGGACCTGGGCTGGAAGTGGATTTCATGAACCCAAGGGCTACCATGCCAATT	1022
Db	1746	ACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCATGCCAATT	1805
Qy	1023	TCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGG	1082
Db	1806	TCTGCCTCGGGCCCTGCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAGGTCCTGG	1865
Qy	1083	CTCTGTACAACCAGCACAAACCGGGCGCGTCCGGCGGCGCCGTGCTGCGTGCCGCAGGCGC	1142
Db	1866	CCCTGTACAACCAGCATAAACCGGGCGCCTCGGCGGCGCCGTGCTGCGTGCCGCAGGCGC	1925
Qy	1143	TGGAGCCACTGCCCATCGTGTACTACGTGGGCGCAAGCCCAAGGTGGAGCAGCTGTCCA	1202
Db	1926	TGGAGCCGCTGCCCATCGTGTACTACGTGGGCGCAAGCCCAAGGTGGAGCAGCTGTCCA	1985
Qy	1203	ACATGATCGTGCGTTCCTGCAAGTGACAGCTGAGGCCCGCCCCGCCACAGCCCCGCCCA	1262
Db	1986	ACATGATCGTGCGTTCCTGCAAGTGACAGCTGAGGTCCCGCCCCGCCCGCCCCGCCCGG	2045

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QY      1263 CCCGGCAGGCCCGGCCCCACCCCGCCCGCCT-----CACCGGGGCTGTATTTAAGG 1314
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2046 CAGGCCCGGCCCCACCCCGCCCCGCCCCGCTGCCTTGCCCATGGGGGCTGTATTTAAGG 2105

QY      1315 ACATCGTGCCCCAAGCCCACTTGGGATCGATTAAA 1349
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      2106 ACACCGTGCCCCAAGCCCACTGGGGCCCCATTAA 2140

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RESULT 5

US-09-948-002-1

; Sequence 1, Application US/09948002

; Publication No. US20030050265A1

; GENERAL INFORMATION:

APPLICANT: Nicholas M. Dean

APPLICANT: Susan F. Murray

; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH

; TITLE OF INVENTION: FACTOR BETA EXPRESSION

FILE REFERENCE: ISPH-0607

; CURRENT APPLICATION NUMBER: US/09/948,002

CURRENT FILING DATE: 2000-09-05

PRIOR APPLICATION NUMBER: 09/661,753

PRIOR FILING DATE: 2000-09-14

; PRIOR APPLICATION NUMBER: 60/154,546

PRIOR FILING DATE: 1999-09-17

; NUMBER OF SEQ ID NOS: 71

; SEO ID NO 1

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; LENGTH: 2094

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;      LENGTH: 2
;      TYPE: DNA

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; ORGANISM: Mus musculus

FEATURE:

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; NAME/KEY: CDS

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; LOCATION: (868) ... (2040)

US-09-948-002-1

Query Match 62.5%; Score 850.2; DB 11; Length 2094;

Best Local Similarity 80.9%; Pred. No. 3.7e-221;

Matches 1040; Conservative 0; Mismatches 188; Indels 57; Gaps 2;

Qy	6	CCGAGATGGCGCCTTCGGGGGCTGCGGCTCTTGCCGCTGCTGCTGCCGCTGCTGTGGCTGC	65
Db	863	CCCCCATGCGCCCTCGGGGCTGCGGCTACTGCCGCTTCTGCTCCCACTCCCGTGGCTTC	922
Qy	66	TAGTGCTGACGCCTGGCCGGCCGGCCGCCGACTGTCCACCTGCAAGACCATCGACATGG	125
Db	923	TAGTGCTGACGCCCGGGAGGCCAGCCGCGGACTCTCCACCTGCAAGACCATCGACATGG	982
Qy	126	AGCTGGTGAAGCGGAAGCGCATCGAGGCCATTCTGCGGCCAGATTCTGTCCAAGCTTCGGC	185
Db	983	AGCTGGTGAACCGGAAGCGCATCGAAGCCATCCGTGGCCAGATCCTGTCCAAACTAAGGC	1042
Qy	186	TTGCCAGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCCGCTGCCTGAGGCAGTACTGG	245
Db	1043	TCGCCAGTCCCCCAAGCCAGGGGGAGGTACCGCCCGGCCCCGCTGCCCGAGGCGGTGCTCG	1102
Qy	246	CTCTTTACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGC	305

Db	1103	CTTTGTACAACAGCACCCGCGACCGGGTGGCAGGCGAGAGCGCCGACCCAGAGCCGGAGC	1162
Qy	306	CAGAGGCGGACTACTACGCCAAGGAGGTCAACCGCGTGCTAATGGTGGAAAGCGGCAACC	365
Db	1163	CCGAAGCGGACTACTATGCTAAAGAGGTCAACCGCGTGCTAATGGTGGACCGCAACAACG	1222
Qy	366	AAATCTATGATAAAATTCAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGG	425
Db	1223	CCATCTATGAGAAAACCAAAGACATCTCACACAGTATATATATGTTCTTCAATACGTCAG	1282
Qy	426	AGCTCCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGA	485
Db	1283	ACATTCCGGGAAGCAGTGCCCGAACCCCATTTGCTGTCCCGTGCGAGCTGCGCTTGCGAGA	1342
Qy	486	GGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCTT	545
Db	1343	GATTAAAATCAAGTGTGGAGCAACATGTGGAACTCTACCAGAAATATAGCAACAATTCTT	1402
Qy	546	GGCGCTACCTCAGCAACCGGCTGCTGGCCCCAGTGACTCACCGGAGTGCGTGTCTTTG	605
Db	1403	GGCGTTACCTTGGTAACCGGCTGCTGACCCCCACTGATACGCTGAGTGCGTGTCTTTG	1462
Qy	606	ATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGCGAGAGGCTATAGAGGGTTTTTCGCC	665
Db	1463	ACGTCACTGGAGTTGTACGGCAGTGGCTGAACCAAGGAGACGGAATACAGGGCTTTCGAT	1522
Qy	666	TCAGTGCCCACTGTTCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGT	725
Db	1523	TCAGCGCTCACTGCTCTGTGACAGCAAAGATAACAAACTCCACGTGGAAATCAACGGGA	1582
Qy	726	TCAATTCTGGCCGCCGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCTGTC	785
Db	1583	TCAGCCCCAAACGTGCGGGCGACCTGGGCACCATCCATGACATGAACCGGCCCTTCTGTC	1642
Qy	786	TCCTCATGGCCACCCCGCTGGAGAGGGCCAGCACCTGCACAGCTCCCGGCACCGCCGAG	845
Db	1643	TCCTCATGGCCACCCCCCTGGAAAGGGCCAGCACCTGCACAGCTCACGGCACCGGAGA-	1701
Qy	846	CCCTGGATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCCTGGATA	905
Db	1702	-----GCCCTGGATA	1711
Qy	906	CCAATACTGCTTCAGCTCCACGAGAAGAACTGCTGCGTGCGGCAGCTCTACATTGACT	965
Db	1712	CCAATAATTGCTTCAGCTCCACAGAGAAGAACTGCTGTGTGCGGCAGCTGTACATTGACT	1771
Qy	966	TCCGGAAGGACCTGGGCTGGAAAGTGGATTATGAACCCAAAGGGCTACCATGCCAATTTCT	1025
Db	1772	TTAGGAAGGACCTGGGTGGAAAGTGGATCCACGAGCCCAAGGGCTACCATGCCAATTTCT	1831
Qy	1026	GCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTC	1085
Db	1832	GTCTGGGACCTGCCCCATATTGGAGCCTGGACACACAGTACAGCAAGGTCCTTGCCC	1891
Qy	1086	TGTACAACCAGCACAACCCGGGCGCGTCCGGCGCGCGTGCTGCGTGCCGCAGGCGCTGG	1145

Db	1892	TCTACAACCAACACAACCCGGGCGCTTCGGCGTCACCGTGCTGCGTGCCGCAGGCTTTGG	1951
Qy	1146	AGCCACTGCCCATCGTGTA	1205
Db	1952	AGCCACTGCCCATCGTCTACTACGTGGGTCGCAAGCCCAAGGTGGAGCAGTTGTCCAACA	2011
Qy	1206	TGATCGTGCGTTCTTGCAAGTGCAGCTGAGGCCCCGCCCCGCCACAGCCCCGCCACCC	1265
Db	2012	TGATTGTGCGCTCTTGCAAGTGCAGCTGAAGCCCCGCCCCG-----CCCGCCCCCTCCC	2065
Qy	1266	GGCAGGCCCCGGCCCCACCCCCGCC	1290
Db	2066	GGCAGGCCCCGGCCCCGCCCCGCC	2090

US-09-948-002-27

; Sequence 27, Application US/09948002

; Publication No. US20030050265A1

; GENERAL INFORMATION:

; APPLICANT: Nicholas M. Dean

; APPLICANT: Susan F. Murray
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH

; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH
 ; TITLE OF INVENTION: FACTOR BETA EXPRESSION

; FILE REFERENCE: ISPH-0607

; CURRENT APPLICATION NUMBER: US/09/948,002

; CURRENT FILING DATE: 2000-09-05

PRIOR APPLICATION NUMBER: 09/661,753

PRIOR FILING DATE: 2000-09-14

;
PRIOR APPLICATION NUMBER: 60/154,546

; PRIOR FILING DATE: 1999-09-17

NUMBER OF SEQ ID NOS: 71

; SEQ ID NO 27

LENGTH: 1585

; TYPE: DNA

ORGANISM: *Rattus norvegicus*

FEATURE:

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; NAME/KEY: CDS

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; LOCATION: (413) ... (1585)

US-09-948-002-27

Query Match 61.0%; Score 830.6; DB 11; Length 1585;

Best Local Similarity 81.3%; Pred. No. 7.4e-216;

Matches 999; Conservative 0; Mismatches 179; Indels 51; Gaps 1;

Qy	6	CCGAGATGGCGCCTTCGGGGCTGCGGCTCTTGCCGCTGCTGCTGCCGCTGCTGTGGCTGC	65
Db	408	CCCCCATGCCGCCCTCGGGGCTGCGGCTGCTGCCGCTTCTGCTCCCACTCCCGTGGCTTC	467
Qy	66	TAGTGCTGACGCCTGGCCGGCCGGCCGCCGACTGTCCACCTGCAAGACCATCGACATGG	125
Db	468	TAGTGCTGACGCCCGGAGGCCAGCCGCGGACTCTCCACCTGCAAGACCATCGACATGG	527
Qy	126	AGCTGGTGAAGCGAAGCGCATCGAGGCCATTGCGGCCAGATTCTGTCCAAGCTTCGGC	185
Db	528	AGCTGGTGAAA CGGAAGCGCATCGAAGCCATCCGTGGCCAGATCCTGTCCA AACTAAGGC	587

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Db 408 CCCCCATGCCGCCCTCGGGGCTGCGGCTGCTGCCGCTTCTGCTCCCACTCCCGTGGCTTC 467

Qv 66 TAGTGCTGACGCTGGCCGGCCGGCCGGACTGTCCACCTGCAAGACCATCGACATGG 125

[illegible]

Db 468 TAGTGCTGACGCCCGGGAGGCCAGCCGCGGGACTCTCCACCTGCAAGACCATCGACATGG 527

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Ov 126 AGCTGGTGAAGCGGAAGCGCATCGAGGCCATTGCGGCCAGATTCTGTCCAAGCTTCGGC 185

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Db 528 AGCTGGTGAAACGGAAGCGCATCGAAGCCATCCGTGGCCAGATCCTGTCCAAACTAAGGC 587

Qy 186 TTGCCAGCCCCCGAGCCAGGGGGACGTGCCGCCCGCCGCTGCCTGAGGCAGTACTGG 245
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 588 TCGCCAGTCCCCGAGCCAGGGGGAGGTACCGCCGGGCCGCTGCCCGAGGCGGTGCTCG 647

Qy 246 CTCTTTACAACAGTACCCGCGACCGGGTAGCCGGGGAAAAGTGTCGAACCGGAGCCCGAGC 305
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 648 CTTTGTACAACAGCACCCGCGACCGGGTGGCAGGCGAGAGCGCTGACCCGAGCCCGAGC 707

Qy 306 CAGAGGCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGAAAGCGGCAACC 365
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 708 CCGAGGCGGACTACTACGCCAAAGAAGTCACCCGCGTGCTAATGGTGACCGCAACAACG 767

Qy 366 AAATCTATGATAAAATTCAAGGGCACCCCCCAGAGCTTATATATGCTGTTCAACACGTCGG 425
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 768 CAATCTATGACAAAACCAAAGACATCACACACAGTATATATATGTTCTTCAATACGTCAG 827

Qy 426 AGCTCCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGA 485
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 828 ACATTCGGGAAGCAGTGCCAGAACCCTTGTCTGCCGTGCAGAGCTGCGCCTGCAGA 887

Qy 486 GGCTCAAGTTAAAAGTGAGCAGCACGTGGAGCTATACCAGAAAATACAGCAATGATTCTCT 545
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 888 GATTCAAGTCAACTGTGGAGCAACACGTAGAACTCTACCAGAAAATATAGCAACAATCTCT 947

Qy 546 GCGCTACCTCAGCAACCGGCTGCTGGCCCCAGTGACTCACCGGAGTGGCTGTCCTTTG 605
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 948 GCGGTTACCTTGGTAACCGGCTGCTGACCCCCACTGATACGCCTGAGTGGCTGTCCTTTG 1007

Qy 606 ATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGAGAGAGGCTATAGAGGGTTTTTCGCC 665
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 1008 ACGTCACTGGAGTTGTCCGGCAGTGGCTGAACCAAGGAGACGGAATACAGGGCTTTTCGCT 1067

Qy 666 TCAGTGCCCACTGTTCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGT 725
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 1068 TCAGTGCTCACTGCTCTGTGACAGCAAAGATAATGTACTCCACGTGGAAATCAATGGGA 1127

Qy 726 TCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCTCTGC 785
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 1128 TCAGTCCCAAACGTGAGGTGACCTGGGCACCATCCATGACATGAACCGACCTTCTCTGC 1187

Qy 786 TCCTCATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAG 845
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 1188 TCCTCATGGCCACCCCCCTGGAAAGGGCTCAACACCTGCACAGCTCCAGGCACCGGAGA- 1246

Qy 846 CCCTGGATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCCTGGATA 905
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 1247 -----GCCCTGGATA 1256

Qy 906 CCAACTACTGCTTCAGTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTCTACATTGACT 965
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 1257 CCAACTACTGCTTCAGTCCACAGAGAAGAACTGCTGTGTACGGCAGCTGTACATTGACT 1316

Qy 966 TCCGGAAGGACCTGGGCTGGAAGTGATTATGAACCCAAGGGCTACCATGCCAATTTCT 1025
 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 1317 TTAGGAAGGACCTGGGTGGAAGTGATTCCACGAGCCAAGGGCTACCATGCCAATTTCT 1376

Qy 1026 GCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTC 1085

Db	1377	GTCTGGGGCCCTGCCCTACATTGGAGCCTGGACACACAGTACAGCAAGGTCCTTGCCC	1436
Qy	1086	TGTACAACCAGCACAAACCCGGGCGCGTCGGCGGCGCCGTGCTGCGTGCCGCAGGCGCTGG	1145
Db	1437	TCTACAACCAACACAAACCCGGGTGCTTCCGCATCACCGTGCTGCGTGCCGCAGGCTTTGG	1496
Qy	1146	AGCCACTGCCCATCGTGTA TACTACGTGGGCGCAAGCCCAAGGTGGAGCAGCTGTCCAACA	1205
Db	1497	AGCCACTGCCCATCGTCTACTACGTGGGTGCGCAAGCCCAAGGTGGAGCAGTTGTCCAACA	1556
Qy	1206	TGATCGTGCGTTCCTGCAAGTGCAGCTGA	1234
Db	1557	TGATCGTGCGTTCCTGCAAGTGCAGCTGA	1585

RESULT 7

US-09-756-283A-19
; Sequence 19, Application US/09756283A
; Patent No. US20020151478A1
; GENERAL INFORMATION:
; APPLICANT: Chernajovsky, Yuti
; APPLICANT: Dreja, Hanna Stina
; APPLICANT: Adams, Gillian
; TITLE OF INVENTION: Latent Fusion Protein
; FILE REFERENCE: 0623.1000000
; CURRENT APPLICATION NUMBER: US/09/756,283A
; CURRENT FILING DATE: 2001-01-09
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 1376
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: LAP-mIFNbeta construct
; NAME/KEY: CDS
; LOCATION: (1)..(1368)
US-09-756-283A-19

Query Match 48.3%; Score 657.2; DB 10; Length 1376;
Best Local Similarity 88.3%; Pred. No. 1e-168;
Matches 726; Conservative 0; Mismatches 93; Indels 3; Gaps 1;

Qy	11	ATGGCGCCTTCGGGGCTGCGGCTCTTGCCGCTGCTGCTGCCGCTGCTGTGGCTGCTAGTG	70
Db	1	ATGCCGCCCTCCGGGCTGCGGCTGCTGCCGCTGCTGCTACCGCTGCTGTGGCTACTGGTG	60
Qy	71	CTGACGCCTGGCCGCGCCGCGCCGCGGACTGTCCACCTGCAAGACCATCGACATGGAGCTG	130
Db	61	CTGACGCCTGGCCGCGCCGCGCGGACTATCCACCTGCAAGACTATCGACATGGAGCTG	120
Qy	131	GTGAAGCGGAAGCGCATCGAGGCCATTGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCC	190
Db	121	GTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCC	180
Qy	191	AGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCGCTGCCTGAGGCAGTACTGGCTCTT	250

```

      |||
Db      181 AGCCCCCGAGCCAGGGGAGGTGCCGCCCGGCCCGCTGCCCGAGGCCGTGCTCGCCCTG 240
Qy      251 TACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCGAGCCAGAG 310
      |||
Db      241 TACAACAGCACCCGCGACCGGGTGCCCGGGGAGAGTGCAGAACCGGAGCCCGAGCCTGAG 300
Qy      311 GCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAGCGGCAACCAAATC 370
      |||
Db      301 GCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAACCCACAACGAAATC 360
Qy      371 TATGATAAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTC 430
      |||
Db      361 TATGACAAGTTCAAGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAGAGCTC 420
Qy      431 CGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCT--GAGG 487
      |||
Db      421 CGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGAGG 480
Qy      488 CTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCCTGG 547
      |||
Db      481 CTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCTGG 540
Qy      548 CGCTACCTCAGCAACCGGCTGCTGGCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGAT 607
      |||
Db      541 CGATACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTGAT 600
Qy      608 GTCACCGGAGTTGTGCGGCAGTGGCTGACCCGAGAGAGGCTATAGAGGGTTTTCGCCTC 667
      |||
Db      601 GTCACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTTCGCCTT 660
Qy      668 AGTGCCCACTGTTCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTC 727
      |||
Db      661 AGCGCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGTTC 720
Qy      728 AATTCTGGCCGCCGGGGTGACCTGGCCACCATTACCGGCATGAACCGGCCCTTCTCTGCTC 787
      |||
Db      721 ACTACCGGCCGCCGAGGTGACCTGGCCACCATTATGGCATGAACCGGCCTTCTCTGCTT 780
Qy      788 CTCATGGCCACCCCGCTGGAGAGGGCCAGCACCTGCACAGC 829
      |||
Db      781 CTCATGGCCACCCCGCTGGAGAGGGCCAGCATCTGCAAAGC 822

```

RESULT 8

US-09-756-283A-21

; Sequence 21, Application US/09756283A

; Patent No. US20020151478A1

; GENERAL INFORMATION:

; APPLICANT: Chernajovsky, Yuti

; APPLICANT: Dreja, Hanna Stina

; APPLICANT: Adams, Gillian

; TITLE OF INVENTION: Latent Fusion Protein

; FILE REFERENCE: 0623.1000000

; CURRENT APPLICATION NUMBER: US/09/756,283A

; CURRENT FILING DATE: 2001-01-09

; NUMBER OF SEQ ID NOS: 100

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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
;   LENGTH: 1352
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: mIFNbeta-LAP construct
;   NAME/KEY: CDS
;   LOCATION: (1)..(1344)
US-09-756-283A-21
```

Query Match 43.7%; Score 594.6; DB 10; Length 1352;
Best Local Similarity 87.3%; Pred. No. 1.1e-151;
Matches 664; Conservative 0; Mismatches 94; Indels 3; Gaps 1;

Qy	73	GACGCTGGCCGGCCGGCCGGGACTGTCCACCTGCAAGACCATCGACATGGAGCTGGT	132
Db	582	GGCGGGAGGGGGCTCAGCGGCCGCACTATCCACCTGCAAGACTATCGACATGGAGCTGGT	641
Qy	133	GAAGCGGAAGCGCATCGAGGCCATTTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCCAG	192
Db	642	GAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCCAG	701
Qy	193	CCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTTTA	252
Db	702	CCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGCTGCCCGAGGCCGTGCTCGCCCTGTA	761
Qy	253	CAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTCGAACCGGAGCCCAGCCAGAGGC	312
Db	762	CAACAGCACCCGCGACCGGGTGGCCGGGGAGAGTGCAGAACCGGAGCCCAGCCTGAGGC	821
Qy	313	GGACTACTACGCCAAGGAGGTACCCGCGTGCTAATGGTGAAAGCGGCAACCAAATCTA	372
Db	822	CGACTACTACGCCAAGGAGGTACCCGCGTGCTAATGGTGAAACCCACAACGAAATCTA	881
Qy	373	TGATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTCCG	432
Db	882	TGACAAGTTCAAGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAGAGCTCCG	941
Qy	433	GGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCT--GAGGCT	489
Db	942	AGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGAGGCT	1001
Qy	490	CAAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCTGGCG	549
Db	1002	CAAGTTAAAAGTGGAGCAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCTGGCG	1061
Qy	550	CTACCTCAGCAACCGGCTGCTGGCCCCAGTGACTACCCGAGTGCGCTGTCTTTGATGT	609
Db	1062	ATACCTCAGCAACCGGCTGCTGGCACCAGCGACTCGCCAGAGTGTTATCTTTTGATGT	1121
Qy	610	CACCGGAGTTGTGCGGCAGTGGCTGACCCGAGAGAGGCTATAGAGGGTTTTCGCCTCAG	669
Db	1122	CACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGAGGGGAAATTGAGGGCTTTTCGCCTTAG	1181
Qy	670	TGCCCACTGTTTCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAA	729

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Db      1182 CGCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGGTTCAC 1241
Qy      730 TTCTGGCCGCCGCGGGGTGACCTGGCCACCATTACGGCATGAACCGGCCCTTCCTGCTCCT 789
      | | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1242 TACCGGCCGCCGAGGTGACCTGGCCACCATTATGGCATGAACCGGCCCTTCCTGCTTCT 1301
Qy      790 CATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCT 830
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1302 CATGGCCACCCCGCTGGAGAGGGCCCAGCATCTGCAAAGCT 1342

```

RESULT 9

US-09-911-904-167

```

; Sequence 167, Application US/09911904
; Publication No. US20030096234A1
; GENERAL INFORMATION:
; APPLICANT: Farr, Spencer B.
; APPLICANT: Pickett, Gavin G.
; APPLICANT: Neft, Robin Eileen
; APPLICANT: Dunn, II, Robert Thomas
; TITLE OF INVENTION: CANINE TOXICITY GENES
; FILE REFERENCE: 400742000200
; CURRENT APPLICATION NUMBER: US/09/911,904
; CURRENT FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/220,057
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 386
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 167
; LENGTH: 489
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(489)
; OTHER INFORMATION: n = A, T, C or G
US-09-911-904-167

```

```

Query Match          26.0%; Score 354.4; DB 11; Length 489;
Best Local Similarity 84.1%; Pred. No. 1.8e-86;
Matches 445; Conservative 0; Mismatches 32; Indels 52; Gaps 2;

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Qy      774 GGCCCTTCCTGCTCCTCATGGCCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCC 833
      | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1 GACCCTTCCTGCTCCTCATGGCCACCCCACTGGAGAGGGCCCAGCACCTGCACAGCTCCC 60
Qy      834 GGCACCGCCGAGCCCTGGATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTC 893
      |||| |||||
Db      61 GGCAGCGCCG----- 70
Qy      894 TGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGC 953
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      71 -GGCCCTGGACACCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTCCGGCAGC 129
Qy      954 TCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTTCATGAACCCAAGGGCTACC 1013
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      130 TCTACATTGACTTCCGCAAGGATCTGGGCTGGAAGTGGATCCATGAGCCCAAGGGTTACC 189

```

[illegible]

US-09-813-271B-1

; Sequence 1, Application US/09813271B

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: New process for the production of
biologically active protein

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. US20020115834A1artis Patent Department

STREET: 564 Morris Avenue

CITY: Summit

STATE: New Jersey

COUNTRY: USA

ZIP: 07901

COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Floppy disk

```

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; COMPUTER: IBM PC compatible

```

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; OPERATING SYSTEM: PC-DOS/MS-DOS
```

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; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

```

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; CURRENT APPLICATION DATA:

```

APPLICATION NUMBER: US/09/813,271B

FILING DATE: 20-Mar-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP95/02719

FILING DATE: 12-Jul-95

APPLICATION NUMBER: EPO 94810439.3

FILING DATE: 25-Jul-94

ATTORNEY/AGENT INFORMATION:

NAME: Pfeiffer, Hesna J.

REGISTRATION NUMBER: 22640

REFERENCE/DOCKET NUMBER: 4-20039C/C1C1/USN

; TELECOMMUNICATION INFORMATION:

```

;           TELEPHONE: (908) 522-6940
;           TELEFAX: (908) 522-6955
;   INFORMATION FOR SEQ ID NO: 1:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 339 base pairs
;           TYPE: nucleic acid
;           STRANDEDNESS: double
;           TOPOLOGY: linear
;       MOLECULE TYPE: cDNA to mRNA
;       HYPOTHETICAL: NO
;       IMMEDIATE SOURCE:
;           CLONE: E. coli LC137/pPLMu.hTGF-beta1 (DSM 5656)
;       FEATURE:
;           NAME/KEY: CDS
;           LOCATION: 1..336
;           OTHER INFORMATION: /product= "human TGF-beta1"
;       SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-813-271B-1

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```

Query Match          22.7%;   Score 308.6;   DB 10;   Length 339;
Best Local Similarity 94.4%;   Pred. No. 4.6e-74;
Matches 320;   Conservative 0;   Mismatches 19;   Indels 0;   Gaps 0;

```

```

Qy      896  GCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTC 955
          |||
Db      1    GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTG 60

Qy      956  TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTGATGAACCCAAGGGCTACCAT 1015
          |||
Db      61   TACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCAT 120

Qy     1016  GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 1075
          |||
Db     121   GCCAATTTCTGCCTCGGGCCCTGCCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAG 180

Qy     1076  GTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGCTCGGCGGGCGCCGTGCTGCGTGCCG 1135
          |||
Db     181   GTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCTCGGCGGGCGCCGTGCTGCGTGCCG 240

Qy     1136  CAGGCGCTGGAGCCACTGCCCCATCGTGTACTACGTGGGCGGCAAGCCCAAGGTGGAGCAG 1195
          |||
Db     241   CAGGCGCTGGAGCCGCTGCCCCATCGTGTACTACGTGGGCGGCAAGCCCAAGGTGGAGCAG 300

Qy     1196  CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 1234
          |||
Db     301   CTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGA 339

```

RESULT 11

US-09-906-158-3

; Sequence 3, Application US/09906158

; Publication No. US20030078217A1

; GENERAL INFORMATION:

; APPLICANT: Brett P. Monia

; APPLICANT: Susan M. Freier

; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR-BETA 3
EXPRESSION

; FILE REFERENCE: RTS-0257
; CURRENT APPLICATION NUMBER: US/09/906,158
; CURRENT FILING DATE: 2001-07-14
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 3
; LENGTH: 2574
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (254)...(1492)
US-09-906-158-3

Query Match 18.3%; Score 249; DB 11; Length 2574;
Best Local Similarity 53.5%; Pred. No. 1.2e-57;
Matches 668; Conservative 0; Mismatches 530; Indels 51; Gaps 5;

```
Qy      36 TGCCGCTGCTGCTGCCGCTGCTGTGGCTGCTAGTGCTGACGCCTGGCCGGCCGGCCGCCG 95
      ||| ||| | | ||| || ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      261 TGCACCTGCAAAGGGCTCTGGTGGTCTGGCCCTGCTGAACTTTGCCACGGTCAGCCTCT 320

Qy      96 GACTGTCCACCTGCAAGACCATCGACATGGAGCTGGTGAAGCGGAAGCGCATCGAGGCCA 155
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      321 CTCTGTCCACTTGCAACACCTTGGACTTCGGCCACATCAAGAAGAAGAGGGTGAAGCCA 380

Qy     156 TTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCCAGCCCCCGAGCCAGGGGGACGTGC 215
      || | || |||| || ||||| |||| ||||| ||||| ||||| ||||| |||||
Db      381 TTAGGGGACAGATCTTGAGCAAGCTCAGGCTCACCAGCCCCCTGAGCCAACGGTGATGA 440

Qy     216 CGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTTTACAACAGTACCCGCGACCGGGTAG 275
      || ||| ----- ||| | ||| ||||| ||||| ||||| ||||| ||||| |||||
Db      441 CCCACG-----TCCCCATACAGGTCTGGCCCTTTACAACAGCACCCGGGAGCTGCTGG 494

Qy     276 CCGGGGAAAGTGTCGAACCGGAGCCCG-----AGCCAGAGGCGGACTACT 320
      || | || || |||| | ||| ||||| ||||| ||||| ||||| ||||| |||||
Db      495 AGGAGATGCATGGGGAGAGGGAGGAAGGCTGCACCCAGGAAAACACCGAGTCGGAATACT 554

Qy     321 ACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATCTATGATAAAT 380
      | ||||| || || | |||| | ||| | ||| | ||| | ||| | ||| | |||
Db      555 ATGCCAAAGAAATCCATAAATTCGACATGATCCAGGGGCTGGCGGAGCACAACTGGA 614

Qy     381 TCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTCCGGGAAGCGG 440
      || | || | || | || | || | || | || | || | || | || | || | || |
Db      615 CTGTCTGCCCTAAAGGAATTACCTCCAAGGTTTTCCGCTTCAATGTGTCCTCAGTGGAGA 674

Qy     441 TGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTCAAGTTAAAG 500
      | | | | | || | || | || | || | || | || | || | || | || | || |
Db      675 AAAATAGAACCAACCTATTCCGAGCAGAATTCCGGGTCTTGCGGTGCCCAACCCAGCT 734

Qy     501 TGGAGCAGCACGTGGAG-----CTATACCAGAAATACAGCAATG 539
      ||| | | | | || | || | || | || | || | || | || | || | || |
Db      735 CTAAGCGGAATGAGCAGAGGATCGAGCTCTTCCAGATCCTTCGGCCAGATGAGCACATTG 794

Qy     540 ATTCCTGGCGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGAICTACCGGAGTGGCTGT 599
      ||||| || | || | || | || | || | || | || | || | || | || | || |
Db      795 CCAAACAGCGCTATATCGGTGGCAAGAATCTGCCACACGGGGCACTGCCGAGTGGCTGT 854
```

Qy 600 CCTTTGATGTCACCGGAGTTGTGCGGCAGTGGCTGACCCGAGAGAGGCTATAGAGGGTT 659
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 855 CCTTTGATGTCAGTACTGTCGTGAGTGGCTGTTGAGAAGAGAGTCCAACCTTAGGTC 914

Qy 660 TTCGCCTCAGTGCCCACTGTTCTGTGACAGCAAAGATAACA-----CACTCCACGTGG 713
 | |||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 915 TAGAAATCAGCATTCACTGTCCATGTACACCTTTCAGCCCAATGGAGATATCCTGGAAA 974

Qy 714 AAATTAACGGGTTCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTACGGCATGAACC 773
 | |||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 975 ACATTACGAGGTGATGAAATCAAATTCAAAGGCGTGGACAATGAGGATGACCATGGCC 1034

Qy 774 GGCCCTTCCTGCTCCTCATGGCCACCCCGCTGGAGAGGGCCAGCACCTGCACAGCTCCC 833
 | |||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1035 GTGGAGATCTGGGGCGCCT---CAAGAAGCAGAAGGATCACCACAACCCTCATCTAATCC 1091

Qy 834 GGCACCGCCGAGCCCTGGATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTC 893
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1092 TCATGATGATTCCCCCACACCGGCTCGACAACCCGGGCCAGGGGGGTGAGAGGAAGAAGC 1151

Qy 894 TGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGC 953
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1152 GGGCTTTGGACACCAATTACTGCTTCCGCAACTTGGAGGAGAAGTCTGTGTGCGCCCCC 1211

Qy 954 TCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTTCATGAACCCAAGGGCTACC 1013
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1212 TCTACATTGACTTCCGACAGGATCTGGGCTGGAAGTGGGTCCATGAACCTAAGGGCTACT 1271

Qy 1014 ATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCA 1073
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1272 ATGCCAACTTCTGCTCAGGCCCTTGCCCATACCTCCGAGTGCAGACACAACCCACAGCA 1331

Qy 1074 AGGTCCTGGCTCTGTACAACCAGCACAAACCCGGGCGCGTCGGCGGCGCCGTGCTGCGTGC 1133
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1332 CGGTGCTGGGACTGTACAACACTCTGAACCCTGAAGCATCTGCCTCGCCTTGCTGCGTGC 1391

Qy 1134 CGCAGGCGCTGGAGCCACTGCCCATCGTGTAACGTGGGCGCAAGCCCAAGGTGGAGC 1193
 | |||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1392 CCCAGGACCTGGAGCCCTGACCATCCTGTACTATGTTGGGAGGACCCCCAAAGTGGAGC 1451

Qy 1194 AGCTGTCCAACATGATCGTGCGTTCCTGCAAGTGCAGCTGAGGCCCCGC 1242
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 1452 AGCTCTCCAACATGGTGCTGAAGTCTTGTAATGTAGCTGAGACCCAC 1500

RESULT 12

US-10-028-158-20

; Sequence 20, Application US/10028158

; Publication No. US20020110833A1

; GENERAL INFORMATION:

; APPLICANT: Caniggia, Isabella

; APPLICANT: Post, Martin

; APPLICANT: Lye, Stephen

; TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF

; TITLE OF INVENTION: TROPHOBLAST

; FILE REFERENCE: 11757.38USWO

; CURRENT APPLICATION NUMBER: US/10/028,158

```

; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US/09/380,662
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: PCT/CA98/00180
; PRIOR FILING DATE: 1998-03-05
; PRIOR APPLICATION NUMBER: US 60/039,919
; PRIOR FILING DATE: 1997-03-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 2574
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (254)..(1492)
US-10-028-158-20

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Query Match          18.3%;  Score 249;  DB 13;  Length 2574;
Best Local Similarity 53.5%;  Pred. No. 1.2e-57;
Matches 668;  Conservative 0;  Mismatches 530;  Indels 51;  Gaps 5;

```

```

Qy      36  TGCCGCTGCTGCTGCCGCTGCTGTGGCTGCTAGTGCTGACGCCTGGCCGGCCGGCCGCCG 95
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Qy     156  TTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCCAGCCCCCGAGCCAGGGGGACGTGC 215
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Db      381  TTAGGGGACAGATCTTGAGCAAGCTCAGGCTCACCAGCCCCCTGAGCCAACGGTGATGA 440

Qy     216  CGCCCGGCCCGCTGCCTGAGGCAGTACTGGCTCTTTACAACAGTACCCGCGACCGGGTAG 275
      |  |  ||  |  ||  |  ||  |||  |||  |||  |||  |||  |||  |||  |||
Db      441  CCCACG-----TCCCCTATCAGGTCTGGCCCTTTACAACAGCACCCGGGAGCTGCTGG 494

Qy     276  CCGGGGAAAGTGTGGAACCGGAGCCCG-----AGCCAGAGGCGGACTACT 320
      |  |  ||  ||  |||  ||  |  |  |||  |||  |||  |||  |||  |||
Db      495  AGGAGATGCATGGGGAGAGGGAGGAAGGCTGCACCCAGGAAAACACCGAGTCGGAATACT 554

Qy     321  ACGCCAAGGAGGTACCCCGGTGCTAATGGTGGAAAGCGGCAACCAAATCTATGATAAAT 380
      |  ||||  ||  ||  |  |||  ||  ||  |  ||  |  ||  |  ||  ||
Db      555  ATGCCAAAGAAATCCATAAATTTCGACATGATCCAGGGGCTGGCGGAGCACAACGAACCTGG 614

Qy     381  TCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTCCGGGAAGCGG 440
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RESULT 13
US-09-957-458B-9
; Sequence 9, Application US/09957458B
; Publication No. US20030166271A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Una
; TITLE OF INVENTION: Method for growing stem cells

RESULT 13

US-09-957-458B-9

; Sequence 9, Application US/09957458B

; Publication No. US20030166271A1

: GENERAL INFORMATION:

APPLICANT: Chen, Una

; TITLE OF INVENTION: Method for growing stem cells

; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR-BETA 3
EXPRESSION
; FILE REFERENCE: RTS-0257
; CURRENT APPLICATION NUMBER: US/09/906,158
; CURRENT FILING DATE: 2001-07-14
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 10
; LENGTH: 2879
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (611)...(1843)
US-09-906-158-10

Query Match 17.6%; Score 239.6; DB 11; Length 2879;
Best Local Similarity 53.0%; Pred. No. 4.4e-55;
Matches 658; Conservative 0; Mismatches 539; Indels 45; Gaps 5;

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Qy	779	TTCCTGCTCCTCATGGCCACCCCGCTGGAGAGGGGCCAGCACCTGCACAGCTCCCGGCAC	838
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Qy	957	ACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTTCATGAACCCAAGGGCTACCATG	1016
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RESULT 15

US-09-813-271B-7

; Sequence 7, Application US/09813271B

; Patent No. US20020115834A1

; GENERAL INFORMATION:

; APPLICANT:

; (A) Nico Cerletti

; TITLE OF INVENTION: New process for the production of
; biologically active protein


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;      NUMBER OF SEQUENCES: 13
;      CORRESPONDENCE ADDRESS:
;          ADDRESSEE: No. US20020115834Alartis Patent Department
;          STREET: 564 Morris Avenue
;          CITY: Summit
;          STATE: New Jersey
;          COUNTRY: USA
;          ZIP: 07901
;      COMPUTER READABLE FORM:
;          MEDIUM TYPE: Floppy disk
;          COMPUTER: IBM PC compatible
;          OPERATING SYSTEM: PC-DOS/MS-DOS
;          SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
;      CURRENT APPLICATION DATA:
;          APPLICATION NUMBER: US/09/813,271B
;          FILING DATE: 20-Mar-2001
;      PRIOR APPLICATION DATA:
;          APPLICATION NUMBER: PCT/EP95/02719
;          FILING DATE: 12-Jul-95
;          APPLICATION NUMBER: EPO 94810439.3
;          FILING DATE: 25-Jul-94
;      ATTORNEY/AGENT INFORMATION:
;          NAME: Pfeiffer, Hesna J. .
;          REGISTRATION NUMBER: 22640
;          REFERENCE/DOCKET NUMBER: 4-20039C/C1C1/USN
;      TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (908) 522-6940
;          TELEFAX: (908) 522-6955
;      INFORMATION FOR SEQ ID NO: 7:
;          SEQUENCE CHARACTERISTICS:
;              LENGTH: 336 base pairs
;              TYPE: nucleic acid
;              STRANDEDNESS: double
;              TOPOLOGY: linear
;          MOLECULE TYPE: other nucleic acid
;          DESCRIPTION: /desc = "recombinant hybrid DNA of
;          IMMEDIATE SOURCE:
;              CLONE: E. coli LC137/pPLMu.TGF-beta1(44/45)beta3
;          FEATURE:
;              NAME/KEY: mat_peptide
;              LOCATION: 1..132
;              OTHER INFORMATION: /product= "N-terminal 44 amino
;              acids of human TGF-beta1"
;          FEATURE:
;              NAME/KEY: mat_peptide
;              LOCATION: 133..336
;              OTHER INFORMATION: /product= "C-terminal 68 amino
;              acids of human TGF-beta3"
;          FEATURE:
;              NAME/KEY: CDS
;              LOCATION: 1..336
;              OTHER INFORMATION: /product= "hybrid TGF-beta named
;              TGF-beta1-3"
;          SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-813-271B-7

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Query Match

16.7%; Score 227.2; DB 10; Length 336;

Best Local Similarity 79.8%; Pred. No. 6.2e-52;
Matches 268; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

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Db      1 GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTG 60

Qy      956 TACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTTCATGAACCCAAGGGCTACCAT 1015
          |||
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Qy     1016 GCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAG 1075
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Qy     1076 GTCCTGGCTCTGTACAACACAGCACAAACCCGGGCGCGTCCGGCGGCGCCGTGCTGCGTGCCG 1135
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Db     181 GTGCTGGGACTGTACAACACTCTGAACCCCTGAAGCATCTGCCTCGCCTTGCTGCGTGCCC 240

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Db     241 CAGGACCTGGAGCCCCCTGACCATCCTGTACTATGTTGGGAGGACCCCCAAAGTGGAGCAG 300

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Job time : 411.672 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 10:47:27 ; Search time 3377.39 Seconds
(without alignments)
9794.056 Million cell updates/sec

Title: US-10-017-372E-38
Perfect score: 1361
Sequence: 1 tggtagcgagatggcgccctt.....cgattaaagcggccgcgact 1361

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_htc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pln:*
- 20: em_gss_vrt:*
- 21: em_gss_fun:*
- 22: em_gss_mam:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_rod:*
- 26: em_gss_phg:*
- 27: em_gss_vrl:*
- 28: gb_gss1:*
- 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	4	690.6	50.7	983	13	BX335351	BX335351 BX335351	
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	11	565.8	41.6	717	10	BE260971	BE260971 601153715	
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ALIGNMENTS

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DEFINITION AGENCOURT_6562032 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5745463
5', mRNA sequence.

ACCESSION BM562135

VERSION BM562135.1 GI:18807966

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1072)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation


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Db      380 GCTCAAGTTAAAAAGTGGAGCAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCCTG 439
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Qy      1145 GAGCCACTGCCCAT--CGTGTAACGTGGGCGCG--AAGCCCAAGGTGGAGCAGCTGTC 1200
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Db      1050 CCACAT 1055

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RESULT 2

BX355682/c

LOCUS BX355682 1201 bp mRNA linear EST 05-MAY-2003
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 clone CS0DI002YJ05 3-PRIME, mRNA sequence.
 ACCESSION BX355682

VERSION BX355682.1 GI:30371987
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1201)
 AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 9160.r For
 more information about this cluster, see
[http://www.genoscope.cns.fr/](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DI002CE03NP1&cluster=9160.r)
[cgi-bin/cluster.cgi?seq=CS0DI002CE03NP1&cluster=9160.r](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DI002CE03NP1&cluster=9160.r). Contact :
 Feng Liang Email : fliang@lifetech.com URL :
<http://fulllength.invitrogen.com/> InVitroGen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0DI002CE03NP1.

FEATURES Location/Qualifiers
 source 1..1201
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DI002YJ05"
 /tissue_type="PLACENTA COT 25-NORMALIZED"
 /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and cloned into the Not I and EcoR V
 sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 198 a 326 c 386 g 253 t 38 others
 ORIGIN

Query Match 51.6%; Score 701.6; DB 13; Length 1201;
 Best Local Similarity 82.1%; Pred. No. 5.1e-143;
 Matches 904; Conservative 8; Mismatches 124; Indels 65; Gaps 7;

Qy 260 ACCCGCGACCGGGTAGCCGGGGAAAGTGTCTGAACCGGAGCCCGAGCCAGAG-GCGGACTA 318
 | ||||| ||||| ||||| | :| ||||| ||||| ||| ||: |||
 Db 1046 AACCGCGACCGGGTGGCCGGG--AGAKKCAGAACCGGAGCCCGAGCCTGAGCCCGRACTA 989
 Qy 319 CTACGCCAAGGAGGTCAACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATCTATGATAA 378
 ||||| ||||| :||| ||||| ||||| ||||| ||||| |||||
 Db 988 CTACGCCAAGGAGGTMACCCGCGTGCTAATGGTGGAAACCCACAACGAAATCTATGACAA 929
 Qy 379 ATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTCCGGGAAGC 438
 ||||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 928 GTTCAAGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAGAGCTCCGAGAAGC 869
 Qy 439 GGTGCCGGAACCTGTATTGCTCT-CTCGGGCAGAGCTGCGCCTGCTGAGGCTCAAGTTAA 497
 ||| || ||||| || ||||| | ||||| ||||| ||||| ||||| |||||
 Db 868 GGTACCTGAACCCGTGTTGCTCTCCCCGGGCAGAGCTGCGTCTGCTGAGGCTCAAGTTAA 809

Qy	498	AAGTGGAGCAGCACGTGGAGCTATACCAGAAAATACAGCAATGATTTCCTGGCGCTACCTCA	557
Db	808	AAGTGGAGCAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCTCTGGCGATACCTCA	749
Qy	558	GCAACCGGCTGCTGGCCCCCAGTGACTACCGGAGTGGCTGTCTTTGATGTACCGGAG	617
Db	748	GCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTGATGTACCGGAG	689
Qy	618	TTGTGCGGCAGTGGCTGACCCGAGAGAGGCTATAGAGGGTTTTTCGCCTCAGTGCCCACT	677
Db	688	TTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGA-GGCTTTTCGCCTTAGCGCCCACT	630
Qy	678	GTTCTGTGTACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAATTCTGGCC	737
Db	629	GCTCCTGTGTACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGTTCACTACCGGCC	570
Qy	738	GCCGGGGTGACCTGGCCACCATTACGGCATGAACCGGCCCTTCTGCTCCTCATGGCCA	797
Db	569	GCCGAGGTGACCTGGCCACCATTATGGCATGAACCGGCCCTTCTGCTTCTCATGGCCA	510
Qy	798	CCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGCCCTGGATACCA	857
Db	509	CCCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGCCGAGCCCTGGAC----	454
Qy	858	ACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCCTGGATACCAACTACTGCT	917
Db	453	-----ACCAACTATTGCT	441
Qy	918	TCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACC	977
Db	440	TCAGCTCCACGGAGAAGNACTGCTGCGTGCGGCAGCTGTACATTGACTTCCGCAAGGACC	381
Qy	978	TGGGCTGGAAGTGGATTATGAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCT	1037
Db	380	TCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCATGCCAATTTCTGCCTCGGGCCCT	321
Qy	1038	GTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGTCTCTGGCTCTGTACAACCAGC	1097
Db	320	GCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAGTCTCTGGCCCTGTACAACCAGC	261
Qy	1098	ACAACCCGGGCGCGTCTGGCGGCGCCGTGCTGCGTGCCGAGGCGCTGGAGCCACTGCCCA	1157
Db	260	ATAACCCGGGCGCCTCTGGCGGCGCCGTGCTGCGTGCCGAGGCGCTGGAGCCGCTGCCCA	201
Qy	1158	TCGTGTACTACGTGGGCGCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTT	1217
Db	200	TCGTGTACTACGTGGGCGCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCT	141
Qy	1218	CCTGCAAGTGCAGCTGAGGCCCGCCCCGCCACAGCCCCGCCCAACCGGCAGGCCCGGC	1277
Db	140	CCTGCAAGTGCAGCTGAGGTCCCGCCCCGCCCGCCCCGCCCGCAGGCCCGGCCCCAC	81
Qy	1278	CCCACCCCGCCCGCCT-----CACCGGGGCTGTATTTAAGGACATCGTGCCCCAAG	1329
Db	80	CCCGCCCCGCCCGCCTTGCCCATGGGGGCTGTATTTAA-GACACCGTCCCCAAG	22
Qy	1330	CCCACTTGGGATCGATTAAAG	1350

Qy	66	TAGTGTGACGCCTGGCCCGGCCGCGACTGTCCACCTGCAAGACCATCGACATGG	125
Db	90	TGGTGCTGACGCCTGGCCCGGCCGCGGACTATCCACCTGCAAGACTATCGACATGG	149
Qy	126	AGCTGGTGAAGCGGAAGCGCATCGAGGCCATTTCGCGGCCAGATTCTGTCCAAGCTTCGGC	185
Db	150	AGCTGGTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGC	209
Qy	186	TTGCCAGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGG	245
Db	210	TCGCCAGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGCTGCCCGAGGCCGTGCTCG	269
Qy	246	CTCTTTACAACAGTACCCGCGACCGGGTAGCCGGGGAAAGTGTGAAACCGAGCCCGAGC	305
Db	270	CCCTGTACAACAGCACCCGCGACCGGGTGGCCGGGGAGAGTGCAGAACCGAGCCCGAGC	329
Qy	306	CAGAGGCGGACTACTACGCCAAGGAGGTACCCGCGTGCTAATGGTGGAAAGCGGCAACC	365
Db	330	CTGAGGCCGACTACTACGCCAAGGAGGTACCCGCGTGCTAATGGTGGAAACCCACAACG	389
Qy	366	AAATCTATGATAAAATTAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCCG	425
Db	390	AAATCTATGACAAGTTCAAGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAG	449
Qy	426	AGCTCCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGA	485
Db	450	AGCTCCGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGA	509
Qy	486	GGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCT	545
Db	510	GGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCT	569
Qy	546	GGCGCTACCTCAGCAACCGGCTGCTGGCCCCAGTGACTCACCGGAGTGGCTGTCTTTTG	605
Db	570	GGCGATACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTATCTTTTG	629
Qy	606	ATGTCACCGGAGTTGTGCGGCAGTGCGTACCCGCAGAGAGGCTATAGAGGGTTTTTCGCC	665
Db	630	ATGTCACCGGAGTTGTGCGGCAGTGCTTGAGCCGTGGAGGGGAAATTGAGGGCTTTTCGCC	689
Qy	666	TCAGTGCCCACTGTTTCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGT	725
Db	690	TTAGCGCCCCTGCTCTCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGT	749
Qy	726	TCAATTCTGGCCGCCGGGTGACCTGGCCACCATTACGGCATGAACCGGCCCTTCTCTGC	785
Db	750	TCACTACCGGCCGCCGAGGTGACCTGGCCACCATTATGGCATGAACCGGCCCTTCTCTGC	809
Qy	786	TCCTCATGGCCACCCCGCTGGAGAGGGCCAGCACCTGCACAGCTCCCGGCACCGCCGAG	845
Db	810	TTCTCATGGCCACCCCGCTGGAGAGGGCCAGCATCTGCAAAGTCCCGGCACCGNCGAG	869
Qy	846	CCCTGGATACCAAC	859
Db	870	CCCTGGNACACCAC	883

RESULT 4

BX335351/c

LOCUS BX335351 983 bp mRNA linear EST 01-MAY-2003

DEFINITION BX335351 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI013YH16 3-PRIME, mRNA sequence.

ACCESSION BX335351

VERSION BX335351.1 GI:30308367

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 983)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 9160.r For more information about this cluster, see

<http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DI013DD08NP1>

&cluster=9160.r. Contact : Feng Liang Email : fliang@lifetech.com

URL : <http://fulllength.invitrogen.com/> InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0DI013DD08NP1.

FEATURES Location/Qualifiers

source

1. .983

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DI013YH16"

/tissue_type="PLACENTA COT 25-NORMALIZED"

/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 170 a 280 c 323 g 203 t 7 others

ORIGIN

Query Match 50.7%; Score 690.6; DB 13; Length 983;

Best Local Similarity 83.6%; Pred. No. 1.2e-140;

Matches 859; Conservative 5; Mismatches 105; Indels 59; Gaps 5;

Qy 278 GGGGAAAGTGTCTGAACCGGAGCCCGAGCCAGAGGCGGACTACTACGCCAAGGAGGTCACC 337

||||| ||||| ||||||||||||||||||| ||||||| ||||||| |||||||

Db 983 GGGGAGAGTGCAGAACCGGAGCCCGAGCCTGAGGCCGACTACTACGCCAAGGAGGTCACC 924

Qy 338 CGCGTGCTAATGGTGGAAAGCGGCAACCAAATCTATGATAAATTCAAGGGCACCCCCAC 397

||||| ||||||| ||||| :| ||||| ||||||| || ||||||| || |||||

Db 923 CGCGTGCTAATGGTGGARACCCACAACGAAATCTATGACAAGTTCAAGCAGAGTACACAC 864

Qy 398 AGCTTATATATGCTGTTCAACACGTCGGAGCTCCGGGAAGCGGTGCCGGAACCTGTATTG 457

||| ||||||| || ||||||| || ||||||| || ||||||| || ||||| || |||

Db 863 AGCATATATATGTTCTTCAACACATCAGAGCTCCGAGAAGCGGTACCTGAACCCGTGTTG 804

Qy	458	CTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTCAAGTTAAAAGTGGAGCAGCACGTGGAG	517
Db	803	CTCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTCAAGTTAAAAGTGGAGCAGCACGTGGAG	744
Qy	518	CTATACCAGAAATACAGCAATGATTCTTGGCGCTACCTCAGCAACCGGCTGCTGGCCCCC	577
Db	743	CTGTACCAGAAATACAGCAACAATYCTTGGCGATACCTCAGCAACCGGCTGCTGGCACCC	684
Qy	578	AGTGACTCACCGGAGTGGCTGTCTTTGATGTACCGGAGTTGTGCGGCAGTGGCTGACC	637
Db	683	AGCGACTCGCCAGAGTGGTTATCTTTTGTATGTACCGGAGTTGTGCGGCAGTGGTTGAGC	624
Qy	638	CGCAGAGAGGCTATAGAGGGTTTTTCGCTCAGTGCCCACTGTTCTGTGACAGCAAAGAT	697
Db	623	CGTGGAGGGGAAATTGA-GGCTTTTCGCTTAGCGCCCACTGCTCCTGTGACAGCAGGGAT	565
Qy	698	AACACACTCCACGTGGAAATTAACGGGTTCAATTCTGGCCGCCGGGGTGACCTGGCCACC	757
Db	564	AACACACTGCAAGTGGACATCAACGGGTTCACTACCGGCCGCCGAGGTGACCTGGCCACC	505
Qy	758	ATTCACGGCATGAACCGGCCCTTCTGCTCCTCATGGCCACCCGCTGGAGAGGGCCAG	817
Db	504	ATTCATGGCATGAACCGGCCCTTCTGCTTCTCATGGCCACCCGCTGGAGAGGGCCAG	445
Qy	818	CACCTGCACAGCTCCCGGCACCGCCGAGCCCTGGATACCAACAGCTACCCATACGACGTG	877
Db	444	CATCTGCAAAGCTCCCGGCACCGCCGAGCCCTGGAC-----	409
Qy	878	CCAGACTACGCATCTCTGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC	937
Db	408	-----ACCAACTATTGCTTCAGCTCCACGGAGAAGAAC	376
Qy	938	TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTAT	997
Db	375	TGCTGCGTGCGGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCAC	316
Qy	998	GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA	1057
Db	315	GAGCCCAAGGGCTACCATGCCAACTTCTGCCTCGGGCCCTGCCCTACATTTGGAGCCTG	256
Qy	1058	GACACTCAGTACAGCAAGGTCTTGGCTCTGTACAACCAGCACAAACCGGGCGCGTGGGCG	1117
Db	255	GACACGCAGTAMMMCAAGGTCTTGGCCMTGTACAACCAGCATAACCC-GGCGCCTCGGCG	197
Qy	1118	GCGCCGTGCTGCGTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC	1177
Db	196	GCGCCGTNGT-CGTGCCGCAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCTGC	138
Qy	1178	AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCTTGCAAGTGCAGCTGAGGC	1237
Db	137	AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTCTTGCAAGTGCAGCTGAGGT	78
Qy	1238	CCCGCCCCGCCACAGCCCCGCCACCCGGCAGGCCCGGCCCAACCCCGCCCCGCCCTCAC	1297
Db	77	CCCGCCCCGCC-----CCGCCCCGCCCGGCAGGCCCGGCCCAACCCCGCCCCGCCCGCG	23

Qy 1298 CGGGGCTG 1305
 | | |
 Db 22 CTGCCTTG 15

RESULT 5

BX324511/c

LOCUS BX324511 1041 bp mRNA linear EST 02-MAY-2003

DEFINITION BX324511 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens
 cDNA clone CS0DC024YD20 3-PRIME, mRNA sequence.

ACCESSION BX324511

VERSION BX324511.1 GI:30332381

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1041)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 9160.r For
 more information about this cluster, see

<http://www.genoscope.cns.fr/>

[cgi-bin/cluster.cgi?seq=CS0AC024DB10NP2&cluster=9160.r](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0AC024DB10NP2&cluster=9160.r). Contact :

Feng Liang Email : fliang@lifetech.com URL :

<http://fulllength.invitrogen.com/> InVitroGen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0AC024DB10NP2.

FEATURES Location/Qualifiers

source

1. .1041

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DC024YD20"

/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"

/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V

sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 176 a 283 c 346 g 219 t 17 others

ORIGIN

Query Match 47.7%; Score 649.2; DB 13; Length 1041;

Best Local Similarity 80.6%; Pred. No. 1.4e-131;

Matches 870; Conservative 10; Mismatches 133; Indels 67; Gaps 8;

Qy 279 GGGAAAGTGTGGAACCGGAGCCCCGAGCCAGAGGCGGACTACTACGCCAAGGAGGTCACCC 338

:| | :| | | | | | | | | | | | | | | :| :| :| | | | |

Db 1022 SGGGAGAKGSAGAACCGGAGCCCCGACCCTRASCCR---ACTAYACCCCAAGRAGTCACCC 966

Qy 339 GCGTGCTAATGGTGGAAAGCGGCAACCAAATCTATGATAAATTCAAGGGCACCCCCACA 398

Db	965	GCCTGYTAATGKT-GAAACCCACAACGAAATCTATGACAAGTTCAAGCAGAGTACACACA	907
Qy	399	GCTTATATATGCTGTTCAACACGTCGGAGCTCCGGGAAGCGGTGCCGGAACCTGTATTGC	458
Db	906	GCATATATATGTTCTTCAACACATCAGAGCTCCGAGAAGCGGTACCTGAACCCGTGTTGC	847
Qy	459	TCTCTC-GGGCAGAGCTGCGCCTGCTGAGGCTCAAGTTAAAAGTGAGCAGCACGTGGAG	517
Db	846	TCTCCCSGGGCAGAGCTGCGTCTGCTGAGGCTCAAGTTAAAAGTGAGCAGCACGTGGAG	787
Qy	518	CTATACCAGAAATACAGCAATGATTCTTGGCGCTACCTCAGCAACCGGCTGCTGGCCCCC	577
Db	786	CTGTACCAGAAATACAGCAACAATTCTTGGCGATACCTCAGCAACCGGCTGCTGGCACCC	727
Qy	578	AGTGACTCACCGGAGTGGCTGTCTTTGATGTACCGGAGTTGTGCGGCAGTGGCTGACC	637
Db	726	AGCGACTCGCCAGAGTGGTTATCTTTTGTGATGTACCGGAGTTGTGCGGCAGTGGTTGAGC	667
Qy	638	CGCAGAGAGGCTATAGAGGGTTTTTCGCCTCAGTGCCCACTGTTCTGTGACAGCAAAGAT	697
Db	666	CGTGGAGGGGAAATTGA-GGCTTTCGCCTTAGCGCCCACTGCTCCTGTGACAGCAGGGAT	608
Qy	698	AACACACTCCACGTGGAAATTAACGGGTTCAATTCTGGCCGCCGGGGTGACCTGGCCACC	757
Db	607	AACACACTGCAAGTGGACATCAACGGGTTCACTACCGGCCGCCGAGGTGACCTGGCCACC	548
Qy	758	ATTACCGGCATGAACCGGCCCTTCTGCTCCTCATGGCCACCCCGCTGGAGAGGGCCAG	817
Db	547	ATTCATGGCATGAACCGGCCCTTCTGCTTCTCATGGCCACCCCGCTGGAGAGGGCCAG	488
Qy	818	CACCTGCACAGCTCCCGGCACCGCCGAGCCCTGGATACCAACAGCTACCCATACGACGTG	877
Db	487	CATCTGCAAAGCTCCCGGCACCGCCGAGCCCTGGAC-----	452
Qy	878	CCAGACTACGCATCTCTGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAAC	937
Db	451	-----ACCAACTATTGCTTCAGCTCCACGGAGAAGAAC	419
Qy	938	TGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTGAT	997
Db	418	TGCTGCGTGCGGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCAC	359
Qy	998	GAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTA	1057
Db	358	GAGCCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGCCCTACATTTGGAGCCTG	299
Qy	1058	GACACTCAGTACAGCAAGGTCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCCGGCG	1117
Db	298	GACACGCAGTACAGCAAGGTCTGGCCCTGTACAACCAGCATAACCC-GGCGCCTCGGCG	240
Qy	1118	GCGCCGTGCTGCGTGCCGCAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCCGC	1177
Db	239	GCGCCGTG-TGCGTGCCGCAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCCGC	181
Qy	1178	AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCTTGCAAGTGCAGCTGAGGC	1237

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Db          180 AAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCTCCTGCAAGTGCAGCTGAGGT 121
Qy          1238 CCCGCCCCGCCACAGCCCCGCCACCCGGCAGGCCCGCCCCACCCCGCCCGCCT~-- 1294
          |||||
Db          120 CCCGCCCCGCCCGCCCCGCCCGGCAGGCCCGCCCCACCCCGCCCGCCCGCTGCC 61
Qy          1295 -----CACCGGGGCTGTATTTAAGGACATCGTGCCCCAAGCCCACTTGGGATCGATTAA 1349
          || |||||
Db          60 TTGCCCATGGGGGCTGTATTTAAGGACACCCGTCCCCAAGCCACCTGGSCACCCAYTAA 1

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RESULT 6

BX434425/c

LOCUS	BX434425	888 bp	mRNA	linear	EST 15-MAY-2003
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DEFINITION BX434425 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE014YE16 3-PRIME, mRNA sequence.

ACCESSION BX434425

VERSION BX434425.1 GI:30779291

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 888)

AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

Invitrogen. This sequence belongs to sequence cluster 9160.r For more information about this cluster, see

<http://www.genoscope.cns.fr/>

cgi-bin/cluster.cgi?seq=CS0BAK028AB08NM1&cluster=9160.r. Contact :

Feng Liang Email : fliang@lifetech.com URL :

<http://fulllength.invitrogen.com/> InVitroGen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0BAK028AB08NM1.

FEATURES	Location/Qualifiers
----------	---------------------

source

1. .888

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/organism="Homo sapiens"
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/mol type="mRNA"
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/db xref="taxon:9606"
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/clone="CS0DE014YE16"
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/tissue type="PLACENTA"

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/clone lib="Homo sapiens PLACENTA"
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/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed

with a NotI-oligo(dT) primer. Five prime end enriched,

double-strand cDNA was digested with Not I and cloned

the Not I and EcoRV sites of the pCMVSPORT 6 vector.

Library was not normalized."

BASE COUNT	156 a	253 c	302 g	176 t	1 others
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ORIGIN

Query Match 44.8%; Score 610.4; DB 13; Length 888;

Best Local Similarity 82.6%; Pred. No. 4e-123;

Matches 772; Conservative 0; Mismatches 102; Indels 61; Gaps 4;

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Qy      428 CTCCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGG 487
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Db      888 CTCCAAAAAGCGGTACCTGAACCTTGTGTCTNCCCGGCAGAGCTGCGTCTGCTGA-G 830

Qy      488 CTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCTTG 547
      ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||
Db      829 CTCAAGTTTAAAATGGAGCAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCTTG 770

Qy      548 CGCTACCTCAGCAACCGGCTGCTGGCCCCAGTGA CTACCGGAGTGGCTGTCCTTTGAT 607
      || ||||| ||||| ||||| || ||||| || ||||| || ||||| ||
Db      769 CGATACCTCAGCAACCGGCTGCTGGCACACAGCGACTCGCCAGAGTGGTTATCTTTTGAT 710

Qy      608 GTCACCGGAGTTGTGCGGCAGTGGCTGACCCGAGAGAGGCTATAGAGGGTTTTTCGCCTC 667
      ||||| ||||| ||||| ||||| || ||||| || ||||| || ||||| ||
Db      709 GTCACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTTCGCCTT 650

Qy      668 AGTGCCCACTGTTCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTC 727
      || ||||| ||||| ||||| ||||| || ||||| || ||||| || ||||| ||
Db      649 AGCGCCCACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGTTC 590

Qy      728 AATTCTGGCCGCCCGGGGTGACCTGGCCACCATTCACGGCATGAACCGGCCCTTCCTGCTC 787
      || | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db      589 ACTACCGGCCGCCGAGGTGACCTGGCCACCATTCATGGCATGAACCGGCCCTTCCTGCTT 530

Qy      788 CTCATGGCCACCCCGCTGGAGAGGGCCAGCACCTGCACAGCTCCCGGCACCGCCGAGCC 847
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db      529 CTCATGGCCACCCCGCTGGAGAGGGCCAGCATCTGCAAAGCTCCCGGCACCGCCGA--- 473

Qy      848 CTGGATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCCTGGATACC 907
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db      472 -----GCCCTGGACACC 461

Qy      908 AACTACTGCTTCAGCTCCACGAGAAGAACTGCTGCGTGCGGCAGCTCTACATTGACTTC 967
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db      460 AACTATTGCTTCAGCTCCACGAGAAGAACTGCTGCGTGCGGCAGCTGTACATTGACTTC 401

Qy      968 CGGAAGGACCTGGGCTGGAAGTGGATTATGAACCCAAGGGCTACCATGCCAATTTCTGC 1027
      || ||||| ||||| ||||| ||||| || ||||| ||||| ||||| ||||| ||
Db      400 CGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTACCATGCCAATTCTGC 341

Qy      1028 CTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTCTG 1087
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db      340 CTCGGGCCCTGCCCCCTACATTGGAGCCTGGACACGCAGTACAGCAAGGTCCTGGCCCTG 281

Qy      1088 TACAACCAGCACAACCCGGGCGCGTCGGCGGCGCCGTGCTGCGTGCCGAGGCGCTGGAG 1147
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db      280 TACAACCAGCATAACCCGGGCGCCTCGGCGGCGCCGTGCTGCGTGCCGAGGCGCTGGAG 221

Qy      1148 CCACTGCCCATCGTGTA CTACGTGGGCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATG 1207
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db      220 CCGTGCCCATCGTGTA CTACGTGGGCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATG 161

Qy      1208 ATCGTGCGTTCTCTGCAAGTGCAGCTGAGGCCCCGCCCCGCCACAGCCCCGCCACCCGG 1267
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||
Db      160 ATCGTGCGTCTCTGCAAGTGCAGCTGAGGTCCCGCCCCGCCCGCCCCGCCCGGCGAGGC 101
```



```
Qy      1268 CAGGCCCCGGCCCCACCCCCGCCCGCCT-----CACCGGGGCTGTATTTAAGGACA-T 1318
          | |||||   |||| ||||  |||  ||           ||  |||||||||||||||||||||
Db       100 CCGGCCCCACCCCGCCCCGCCCGCCTTGCCTTGCCCATGGGGGCTGTATTTAAGGACACC 41

Qy      1319 CGTGCCCCAAGCCCACCTTGGGATCGATTAAAGCGG 1353
          ||||||||||||||||| ||||  | ||||||| ||
Db       40  CGTGCCCCAAGCCCACCTGGGCCCCATTAAAGAGG 6
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RESULT 7

BM555996

LOCUS	BM555996	1043 bp	mRNA	linear	EST 20-FEB-2002
-------	----------	---------	------	--------	-----------------

DEFINITION AGENCOURT_6544437 NIH_MGC_88 Homo sapiens cDNA clone IMAGE:5550039
5', mRNA sequence.

ACCESSION BM555996

VERSION BM555996.1 GI:18796907

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1043)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LAM12261 row: i column: 16

High quality sequence stop: 702.

FEATURES

Location/Qualifiers

source

1. .1043

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/organism="Homo sapiens"
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/mol type="mRNA"
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/db xref="taxon:9606"
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/clone="IMAGE:5550039"
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/tissue type="duodenal adenocarcinoma, cell line"
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```
/lab host="DH10B (phage-resistant)"
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```
/clone lib="NIH MGC 88"
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```
/note="Organ: small intestine; Vector: pCMV-SPORT6;
```

Site 1: NotI; Site 2: SalI; Cloned unidirectionally;

oligo-dT primed. Average insert size 1.767 kb. Library enriched for full-length clones and constructed by Life

Technologies. Note: this is a NIH MGC Library."

BASE COUNT	202 a	329 c	345 g	154 t	13 others
------------	-------	-------	-------	-------	-----------

ORIGIN

Query Match 44.8%; Score 610.2; DB 12; Length 1043;

Best Local Similarity 81.1%; Pred. No. 4.7e-123;

Matches 736; Conservative 0; Mismatches 120; Indels 51; Gaps 1;

Qy	396	ACAGCTTATATATGCTGTTCAACACGTCGGAGCTCCGGGAAGCGGTGCCGGAACCTGTAT	455
Db	1	ACAGCATATATATGTTCTTCAACACATCAGAGCTCCGAGAAGCGGTACCTGAACCCGTGT	60
Qy	456	TGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTCAAGTTAAAAGTGGAGCAGCACGTGG	515
Db	61	TGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTCAAGTTAAAAGTGGAGCAGCACGTGG	120
Qy	516	AGCTATACCAGAAATACAGCAATGATTCTGGCGCTACCTCAGCAACCGGCTGCTGGCCC	575
Db	121	AGCTGTACCAGAAATACAGCAACAATTCTGGCGATACCTCAGCAACCGGCTGCTGGCAC	180
Qy	576	CCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTACACCGGAGTTGTGCGGCAGTGGCTGA	635
Db	181	CCAGCGACTCGCCAGAGTGGTTATCTTTTGATGTACACCGGAGTTGTGCGGCAGTGGTTGA	240
Qy	636	CCCGCAGAGAGGCTATAGAGGGTTTTTCGCCTCAGTGCCCACTGTTCTGTGACAGCAAAG	695
Db	241	GCCGTGGAGGGGAAATTGAGGGCTTTTCGCCTTAGCGCCCACTGCTCCTGTGACAGCAGGG	300
Qy	696	ATAACACACTCCACGTGGAAATTAAACGGGTTCAATTCTGGCCGCCGGGGTGACCTGGCCA	755
Db	301	ATAACACACTGCAAGTGGACATCAACGGGTTCACTACCGGCCGCCGAGGTGACCTGGCCA	360
Qy	756	CCATTACGGCATGAACCGGCCCTTCCTGCTCCTCATGGCCACCCGCTGGAGAGGGCCC	815
Db	361	CCATTGATGGCATGAACCGGCCCTTCCTGCTTCTCATGGCCACCCGCTGGAGAGGGCCC	420
Qy	816	AGCACCTGCACAGCTCCCGGCACCGCCGAGCCCTGGATACCAACAGCTACCCATACGACG	875
Db	421	AGCATCTGCAAAGCTCCCGGCACCGCCGA-----	449
Qy	876	TGCCAGACTACGCATCTCTGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGA	935
Db	450	-----GCCCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAGA	489
Qy	936	ACTGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTC	995
Db	490	ACTGCTGCGTGCGGCAGCTGTACATTGACTTCCGCAAGGACCTCGGCTGGAAGTGGATCC	549
Qy	996	ATGAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCC	1055
Db	550	ACGAGCCCAAGGGCTACCATGCCAATTTCTGCCTCGGGCCCTGCCCCTACATTTGGAGCC	609
Qy	1056	TAGACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGCACAACCCGGGCGCGTCGG	1115
Db	610	TGGACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGCATAACCCGGGCGCCTCGG	669
Qy	1116	CGGCGCCGTGCTGCGTGCCGAGGCGCTGGAGCCACTGCCCATCGTGTACTACGTGGGCC	1175
Db	670	CGGCGCCGTGCTGCGTGCCGAGGCGCTGGAGCCGCTGCCCATCGTGTACTACGTGGGCC	729
Qy	1176	GCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTTCTGCAAGTGCAGCTGAG	1235
Db	730	GCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCTCCTGCAGTGCACCTTGAA	789

Qy 1236 GCCCCGCCCCGCCACAGCCCCGCCACCCGGCAGGCCCGGCCCAACCCCGCCCGCCTC 1295
| | | | | | | | | | | | | | | | | | | | | |
Db 790 GGGTCCGGCCCCCACNCGGNCNNNNNGGNNNGGGGGNCCCCGGCGCCGGGCCCCCGC 849

Qy 1296 ACCGGGG 1302
| | |
Db 850 GGCCCCG 856

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RESULT 8
BX383773/c
LOCUS      BX383773                950 bp      mRNA      linear      EST 08-MAY-2003
DEFINITION BX383773 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
            cDNA clone CS0DK001YA15 3-PRIME, mRNA sequence.
ACCESSION  BX383773
VERSION    BX383773.1  GI:30457168
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
            ORGANISM
            Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1  (bases 1 to 950)
AUTHORS    Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE      Full-length cDNA libraries and normalization
JOURNAL    Unpublished
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 9160.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DK001AA08NP1&cluster=9160.r. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DK001AA08NP1.
FEATURES   Location/Qualifiers
            source                1. .950
                                   /organism="Homo sapiens"
                                   /mol_type="mRNA"
                                   /db_xref="taxon:9606"
                                   /clone="CS0DK001YA15"
                                   /cell_type="HELA CELLS COT 25-NORMALIZED"
                                   /cell_line="HELA"
                                   /clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
                                   /note="1st strand cDNA was primed with a NotI-oligo(dT)
                                   primer. Five prime end enriched, double-strand cDNA was
                                   digested with Not I and cloned into the Not I and EcoR V
                                   sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT 171 a      260 c      312 g      195 t      12 others
ORIGIN

```

Query Match 44.3%; Score 603.2; DB 13; Length 950;
Best Local Similarity 79.4%; Pred. No. 1.5e-121;
Matches 791; Conservative 8; Mismatches 134; Indels 63; Gaps 5;

Qy	353	GAAAGCGGCAACCAAAATCTATGATAAAATTCAAGGGCACCCCCACAGCTTATATATGCTG	412
Db	943	GRAACCCACAACGAAATCTATGACAAGTTCAAGCAGAGMACACACAGCATATATATGTTC	884
Qy	413	TTCAACACGTCGGAGCTCCGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAG	472
Db	883	TTCAAMACATCAGAGCTCCGAGAAGCGGTACCTGVACCCGTGTTGCTCTCCCGGGCAGAG	824
Qy	473	CTGCGCCTGCTGAGGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTATAACCAGAAATAC	532
Db	823	CTGCGTCTGCTGAGGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTGTACCAGAAATAC	764
Qy	533	AGCAATGATTCTGGCGCTACCTCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAG	592
Db	763	AGCAACAATAMCTGGCGTACCTCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAG	704
Qy	593	TGGCTGTCCTTTTGATGTACCGGAGTTGTGCGGCAGTGGCTGACCCGAGAGAGGCTATA	652
Db	703	TGGTTATCTTTTGATGTACCGGAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATT	644
Qy	653	GAGGGTTTTTCGCCTCAGTGCCCACTGTTCTGTGTACAGCAAAGATAACACACTCCACGTG	712
Db	643	GA-GGCTTTTCGCCTTAGCGCCCACTGCTCCTGTTACAGCAGGGATTACACACTGCAAGTG	585
Qy	713	GAAATTAACGGGTTCAATTCTGGCCGCCGGGGTGACCTGGCCACCATTACGGCATGAAC	772
Db	584	GACATCAACGGGTTTACTACCGCCGCCGAGGTGACCTGGCCACCATTATGGCATGAAC	525
Qy	773	CGGCCCTTCTGCTCCTCATGGCCACCCCGCTGGAGAGGGGCCAGCACCTGCACAGCTCC	832
Db	524	CGGCCTTCTGCTTCTCATGGCCACCCCGCTGGAGAGGGGCCAGCATCTGCAAAGCTCC	465
Qy	833	CGGCACCGCCGAGCCCTGGATACCAACAGCTACCCATACGACGTGCCAGACTACGCATCT	892
Db	464	CGGCACCGCCGA-----	453
Qy	893	CTGGCCCTGGATACCAACTACTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAG	952
Db	452	---GCMCTGGACACCAACTATTGCTTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAG	396
Qy	953	CTCTACATTGACTTCCGGAAGGACCTGGGCTGGAAGTGGATTATGAACCCAAGGGCTAC	1012
Db	395	CTGTACATTKACTTCCGCAAGGACCTCGGCTGGAAGTGGATCCACGAGCCCAAGGGCTAC	336
Qy	1013	CATGCCAATTTCTGCCTGGGGCCCTGTCCCTACATCTGGAGCCTAGACACTCAGTACAGC	1072
Db	335	CATGCCGACTTCTGCCTCGGGCCCTGCCCTACATTTGGAGCCTGGACACGCAGTACAGC	276
Qy	1073	AAGGTCCTGGCTCTGTACAACCAGCACAAACCGGGCGCGTGGCGGCGCCGTGCTGCGTG	1132
Db	275	AAGGTCCTGGCGCCTGTACAACCAGCATAACCGGGCGCCTGGCGGCGCCGTG-TGCGTG	217
Qy	1133	CCGCAGGCGCTGGAGCCACTGCCCATCGTGTAATACTGCGGGCCGCAAGCCCAAGGTGGAG	1192
Db	216	CCGCAGGCGCTGGAGCCGTGCCCATCGTGTAATACTGCGGGCKKCAAGCCCAAGGTGGAG	157
Qy	1193	CAGCTGTCCAACATGATCGTGCCTTCTGCAAGTGCAGCTGAGGCCCCGCCCCGCCCA	1252

Db 156 CAGCTGTCCNACATGATCGTGCGCTCCTGCAAGTGCAGCTGAGATCCCGCCCCGCCCGC 97
 Qy 1253 GCCCCGCCACCCGGCAGGCCCGGCCACCCCGCCCGC-----CTCACCGGGGC 1303
 Db 96 CCCGCCCGGAAGGCCGCGGCCCAACCCGCCCGCCCCSCTGCCTTGCCCATGGGGGC 37
 Qy 1304 TGTATTTAAGGA-CATCGTGCCCCAAGCCCACTTGG 1338
 Db 36 TGTATTTAAGNACCCCCCTGGCCCAAGCCCACTTGG 1

RESULT 9

AL530081

LOCUS	AL530081	859 bp	mRNA	linear	EST 23-MAY-2003
-------	----------	--------	------	--------	-----------------

DEFINITION AL530081 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens cDNA clone CS0DD009YM06 5-PRIME, mRNA sequence.

ACCESSION AL530081

VERSION AL530081.2 GI:31067916

KEYWORDS EST.

SOURCE	Homo sapiens (human)
--------	----------------------

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 859)

AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

COMMENT On Feb 13, 2001 this sequence version replaced gi:12793574.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr

was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 9160.r For more information about this cluster, see

<http://www.genoscope.cns.fr/>

cgi-bin/cluster.cgi?seq=CS0DD009BG03QP1&cluster=9160.r. Contact :

Feng Liang Email : fliang@lifetech.com URL :

<http://fulllength.invitrogen.com/> InVitroGen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DD009BG03OP1.

FEATURES	Location/Qualifiers
----------	---------------------

source

1. .859

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/organism="Homo sapiens"
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/mol type="mRNA"
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/db xref="taxon:9606"
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/clone="CS0DD009YM06"
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/tissue type="NEUROBLASTOMA COT 50-NORMALIZED"
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/clone lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"
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/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT	179 a	272 c	257 g	148 t	3 others
------------	-------	-------	-------	-------	----------

ORIGIN

Query Match

42.7%; Score 580.6; DB 9; Length 859;

Best Local Similarity 87.3%; Pred. No. 1.3e-116;
Matches 645; Conservative 2; Mismatches 91; Indels 1; Gaps 1;

Qy		6	CCGAGATGGCGCCTTCGGGGGTGC GGCTCTTGCCGCTGCTGCTGCCGCTGCTGTGGCTGC	65
Db		121	CCCCCATGCGGCCCTCCGGGCTGCGGCTGCTGCTGCTGCTACCGCTGCTGTGGCTAC	180
Qy		66	TAGTGTCTGACGCCTGGCCGGCCGGCCGCGGA CTGTCCACTGCAAGACCATCGACATGG	125
Db		181	TGGTGTCTGACGCCTGGCCGGCCGGCCGCGGA CTATCCACTGCAAGACTATCGACATGG	240
Qy		126	AGCTGGTGAAGCGGAAGCGCATCGAGGCCATT CGCGGCCAGATTCTGTCCAAGCTTCGGC	185
Db		241	AGCTGGTGAAGCGGAAGCGCATCGAGGCCAT CC GCGGCCAGAT CCT GTCCAAGCTGCGGC	300
Qy		186	TTGCCAGCCCCCGAGCCAGGGGGACGTGCCGCC CCGCCC GCTGCCTGAGGCAGTA ACTGG	245
Db		301	TCGCCAGCCCCCGAGCCAGGGGGAGGTGCCGCC CCGCCC GCTGCCCC AGGCGCTGCTCG	360
Qy		246	CTCTTTACAACAGTAGCCCCGCGACCGGGTAG CC GGGGAAAGTGTGCAACCGGAG CCCGAGC	305
Db		361	CCCTGTACAACAGCACCCGCGACCGGGTGGCC GG GAGAGTGAGA ACGGAG CCCGAGC	420
Qy		306	CAGAGGCGGACTACTACGCCAAGGAGGTCA CCCGCG TGCTA ATGGTGGAAAGCGG CA ACC	365
Db		421	CTGAGGCCGACTACTACGCCAAGGAGGTCA CCCGCG TGCTA ATGGTGGAAA CCCACA AC G	480
Qy		366	AAATCTATGATAAA T TCAAAGGGCACCCCCCC ACAGCTTATATATGCTGTTCAAACG TC GG	425
Db		481	AAATCTATGACAAG TTCAAAGCAGAGTACACAC AGCATATATATGTTCTTCAACACATCAG	540
Qy		426	AGCTCCGGGAAGCGGTGCCGGAACCTGTATT GC TCTCTCGGGCAGAGCTGCGCCTGCTGA	485
Db		541	AGCTCCGAGAAGCGGTACCTGAACCCGTGTT GC TCTCCCGGGCAGAGCTGCGTCTGCTGA	600
Qy		486	GGCTCAAGTTAAAAAGTGGAGCAGCACGTGG AGCTATACCAGAAATACAGCAATGATT CCT	545
Db		601	GGCTCAAGTTAAAAAGTGGAGCAGCACGTGG AGCTGTACCAGAAATACAGCAACAATTCCT	660
Qy		546	GGCGCTACCTCAGCAACCGGCTGCTGGCCCCC AGTGA CTCACCGGAGTG -GCTGTCCTTT	604
Db		661	GGCGATACCTCAGCAACCGGCTGCTGGCACCC AGCGACTCGCCAGAGTGTGTTATCTTTT	720
Qy		605	GATGTCACCGGAGTTGTGCGGCAGTGGCTGA CCCGCAGAGAGGCTATAGAGGGTTTTTCGC	664
Db		721	GATGTCACCGGAGTTGTGCGGCAGTKGTTGAG CCGTGGAGGGGAAATTGAGGGCTTTTCGC	780
Qy		665	CTCAGTGCCCACTGTTCTGTGACAGCAAAGATA AACACACTCCACGTGGAAATTAACGGG	724
Db		781	CTTAGCGCCCACTGCTCCTGTGACAGCAGGGATAAACACACTGCAAGTGRACATCAACGGG	840
Qy		725	TTCAATTCTGGCCGCCGGG 743	
Db		841	TTCACTACCGGCCGCCGAG 859	

BE312000
 LOCUS BE312000 713 bp mRNA linear EST 26-OCT-2000
 DEFINITION 601154768F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3510592 5',
 mRNA sequence.
 ACCESSION BE312000
 VERSION BE312000.1 GI:9130128
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 713)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: LLCM195 row: h column: 17
 High quality sequence start: 2
 High quality sequence stop: 713.
 FEATURES
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
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 /tissue_type="neuroblastoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_19"
 /note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(G). Library constructed by Ling Hong
 in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."
 BASE COUNT 157 a 226 c 211 g 119 t
 ORIGIN

Query Match 42.2%; Score 573.8; DB 10; Length 713;
 Best Local Similarity 87.8%; Pred. No. 3.7e-115;
 Matches 626; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

Qy 135 AGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCCAGCC 194
 |||
 Db 1 AGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCCAGCC 60
 Qy 195 CCCCAGCCAGGGGGACGTGCCGCCCCGGCCCCGCTGCCTGAGGCAGTACTGGCTCTTTACA 254
 |||
 Db 61 CCCCAGCCAGGGGGAGGTGCCGCCCCGGCCCCGCTGCCCGAGGCCGTGCTCGCCCTGTACA 120

Qy	255	ACAGTACCCGCGACCCGGGTAGCCGGGGAAAAGTGTGGAACCGGAGCCCGAGCCAGAGGCGG	314
Db	121	ACAGCACCCGCGACCCGGGTGGCCGGGGAGAGTGCAGAACCGGAGCCCGAGCCTGAGGCCG	180
Qy	315	ACTACTACGCCAAGGAGGTACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATCTATG	374
Db	181	ACTACTACGCCAAGGAGGTACCCGCGTGCTAATGGTGGAAACCCACAACGAAATCTATG	240
Qy	375	ATAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGGAGCTCCGGG	434
Db	241	ACAAGTTCAGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAGAGCTCCGAG	300
Qy	435	AAGCGGTGCCGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTCAAGT	494
Db	301	AAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTCAAGT	360
Qy	495	TAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCTGGCGCTACC	554
Db	361	TAAAAGTGGAGCAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCTGGCGATACC	420
Qy	555	TCAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTACCG	614
Db	421	TCAGCAACCGGCTGCTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTTGATGTACCG	480
Qy	615	GAGTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTTCGCCTCAGTGCCC	674
Db	481	GAGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTTCGCCTTAGCGCCC	540
Qy	675	ACTGTTCCCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAATTCTG	734
Db	541	ACTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGTTCACTACCG	600
Qy	735	GCCGCCGGGGTGACCTGGCCACCATTACGGCATGAACCGGCCCTTCTGCTCCTCATGG	794
Db	601	GCCGCCGAGGTGACCTGGCCACCATTATGGCATGAACCGGCCCTTCTGCTTCTCATGG	660
Qy	795	CCACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGCC	847
Db	661	CCACCCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGGCACCGCGAGCC	713

BE260971

DEFINITION 601153715F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3509931 5', mRNA sequence.

VERSION BE260971.1 GI:9132709

SOURCE Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)


```

Db      300 AGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTCAAGTT 359
Qy      496 AAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCTGGCGCTACCT 555
      |||
Db      360 AAAAGTGGAGCAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCTGGCGATACCT 419
Qy      556 CAGCAACCGGCTGCTGGCCCCCAGTGACTCACCGGAGTGGCTGTCCTTTGATGTCACCGG 615
      |||
Db      420 CAGCAACCGGCTGCTGGCACCAGCGACTCGCCAGAGTGGTTATCTTTGATGTCACCGG 479
Qy      616 AGTTGTGCGGCAGTGGCTGACCCGAGAGAGGCTATAGAGGGTTTTCGCCTCAGTGCCCA 675
      |||
Db      480 AGTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTGAGGGCTTTCGCCTTAGCGCCCA 539
Qy      676 CTGTTCTGTGACAGCAAAGATAACACACTCCCGTGGAAATTAACGGGTTCAATTCTGG 735
      |||
Db      540 CTGCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGTTCACTACCGG 599
Qy      736 CCGCCGGGGTGACCTGGCCACCATTACGGCATGAACCGGCCCTTCCTGCTCCTCATGGC 795
      |||
Db      600 CCGCCGAGGTGACCTGGCCACCATTATGGCATGAACCGGCCCTTCCTGCTTCTCATGGC 659
Qy      796 CACCCCGCTGGAGAGGGCCCAGCACCTGCACAGCTCCCGGCACCGCCGAGCCCTGGA 852
      |||
Db      660 CACCCCGCTGGAGAGGGCCCAGCATCTGCAAAGCTCCCGGCACCGCGAGCCCTGGGA 716

```

RESULT 12

BQ675698

LOCUS BQ675698 902 bp mRNA linear EST 15-JUL-2002

DEFINITION AGENCOURT_8036532 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6211917
5', mRNA sequence.

ACCESSION BQ675698

VERSION BQ675698.1 GI:21786532

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 902)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLCM2375 row: c column: 22

High quality sequence stop: 599.

FEATURES Location/Qualifiers

source 1..902

/organism="Homo sapiens"

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6211917"
/tissue_type="epidermoid carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_102"
/note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-cDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies). Note: this is a NIH_MGC Library."

```

```

BASE COUNT      194 a      292 c      255 g      161 t
ORIGIN

```

```

Query Match          41.5%;  Score 565.2;  DB 13;  Length 902;
Best Local Similarity 87.0%;  Pred. No. 3.1e-113;
Matches 621;  Conservative 0;  Mismatches 93;  Indels 0;  Gaps 0;

```

```

Qy      156 TTCGCGGCCAGATTCTGTCCAAGCTTCGGCTTGCCAGCCCCCGAGCCAGGGGGACGTGC 215
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1  TCCGCGGCCAGATCCTGTCCAAGCTGCGGCTCGCCAGCCCCCGAGCCAGGGGGAGGTGC 60

Qy      216 CGCCCGGCCCCGCTGCCTGAGGCAGTACTGGCTCTTTACAACAGTACCCGCGACCGGGTAG 275
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      61 CGCCCGGCCCCGCTGCCCCGAGGCCGTGCTCGCCCTGTACAACAGCACCCGCGACCGGGTGG 120

Qy      276 CCGGGGAAAGTGTCTGAACCGGAGCCCGAGCCAGAGGCGGACTACTACGCCAAGGAGGTCA 335
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      121 CCGGGGAGAGTGCAGAACCGGAGCCCGAGCCTGAGGCGGACTACTACGCCAAGGAGGTCA 180

Qy      336 CCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATCTATGATAAAATTCAAGGGCACCCCCC 395
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      181 CCCGCGTGCTAATGGTGGAAACCCACAACGAAATCTATGACAAGTTCAAGCAGAGTACAC 240

Qy      396 ACAGCTTATATATGCTGTTCAACACGTCGGAGCTCCGGAAGCGGTGCCGGAACCTGTAT 455
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      241 ACAGCATATATATGTTCTTCAACACATCAGAGCTCCGAGAAGCGGTACCTGAACCCGTGT 300

Qy      456 TGCTCTCTCGGGCAGAGCTGCGCCTGCTGAGGCTCAAGTTAAAAGTGGAGCAGCACGTGG 515
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      301 TGCTCTCCCGGGCAGAGCTGCGTCTGCTGAGGCTCAAGTTAAAAGTGGAGCAGCACGTGG 360

Qy      516 AGCTATACCAGAAATACAGCAATGATTCTTGGCGCTACCTCAGCAACCGGCTGCTGGCCC 575
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      361 AGCTGTACCAGAAATACAGCAACAAATCTTGGCGATACCTCAGCAACCGGCTGCTGGCAC 420

Qy      576 CCAGTGACTCACCGGAGTGGCTGTCTTTTGATGTACCCGGAGTTGTGCGGCAGTGCTGA 635
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      421 CCAGCGACTCGCCAGAGTGGTTATCTTTTGATGTACCCGGAGTTGTGCGGCAGTGGTTGA 480

Qy      636 CCCGAGAGAGGCTATAGAGGGTTTTCGCCTCAGTGCCCACTGTTCTGTGACAGCAAAG 695
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      481 GCCGTGGAGGGGAAATTGAGGGCTTTCGCCTTAGCGCCCACTGCTCCTGTGACAGAGGG 540

```

```
Qy      696 ATAAACA CACTCCACG TGGAAAT TAACGGGT TCAATTCT GGC CGC GGCG GTG A CCTGGCCA   755
       ||||| |
Db      541 ATAACA CA CTGCAAG TGACATCA ACGGGTTC ACTACC GC CGC GAGGTGA CCTGGCCA   600
                               *
Qy      756 CCATTCA CGGCATGA ACCGG CCTT TCCTGCT CCTCATG GCCACCC CGCTGG AGAGGGCCC   815
       ||||| |
Db      601 CCATTCA TGGCATGA ACCGG CCTT TCCTGCT CTCATG GCCACCC CGCTGG AGAGGGCCC   660
                                     *
Qy      816 AGCACCT GCACAGCT CCCGGC ACCGCC GAGCCCT GGATAcca acagct acccat   869
       ||||| |
Db      661 AGCATCTGCCAAGCT CCCGGC ACCGCC GAGCCCT GGGACacc acctattgc ctt    714
```

RESULT 13

BI818841

LOCUS	BI818841	925 bp	mRNA	linear	EST 04-OCT-2001
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DEFINITION 603037307F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5178433 5', mRNA sequence.

ACCESSION BI818841

VERSION BI818841.1 GI:15930391

KEYWORDS EST.

SOURCE	Homo sapiens (human)
--------	----------------------

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 925)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cdDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM11444 row: n column: 02

High quality sequence stop: 874.

FEATURES	Location/Qualifiers
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source

1. .925

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/organism="Homo sapiens"
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/mol type="mRNA"
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```
/db xref="taxon:9606"
```

```
/clone="IMAGE:5178433"
```

```
/lab host="DH10B"
```

```
/clone lib="NIH MGC 115"
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```
/note="Organ: pooled brain, lung, testis; Vector:
```

pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA

source anonymous pool of 6 male brains, age range 23-27; 1

male lung, age 27; and 1 male testis, age 69. Library

oligo-dT primed and directionally cloned (EcoRV site is

destroyed upon cloning). Average insert size 1.8

insert size range 1-3 kb. Library is normalized and

enriched for full-length clones and was constructed b

Gruber (Invitrogen). Research Genetics tracking code

021. Note: this is a NIH_MGC Library."
BASE COUNT 170 a 316 c 278 g 161 t
ORIGIN

Query Match 39.5%; Score 537.6; DB 12; Length 925;
Best Local Similarity 87.5%; Pred. No. 3.3e-107;
Matches 611; Conservative 0; Mismatches 84; Indels 3; Gaps 2;

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Qy      6 CCGAGATGGCGCCTTCGGGGCTGCGGCTCTTGCCGCTGCTGCTGCCGCTGCTGTGGCTGC 65
      ||  ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db     146 CCCCCATGCCGCCCTCCGGGCTGCGGCTGCTGCCGCTGCTGCTACCGCTGCTGTGGCTAC 205

Qy     66 TAGTGCTGACGCCTGGCCGGCCGGCCGGGACTGTCCACCTGCAAGACCATCGACATGG 125
      | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db    206 TGGTGCTGACGCCTGGCCGGCCGGCCGGGACTATCCACCTGCAAGACTATCGACATGG 265

Qy    126 AGCTGGTGAAGCGGAAGCGCATCGAGGCCATTCGCGGCCAGATTCTGTCCAAGCTTCGGC 185
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db    266 AGCTGGTGAAGCGGAAGCGCATCGAGGCCATCCGCGGCCAGATCCTGTCCAAGCTGCGGC 325

Qy    186 TTGCCAGCCCCCGAGCCAGGGGGACGTGCCGCCCGGCCCGCTGCCTGAGGCAGTACTGG 245
      | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db    326 TCGCCAGCCCCCGAGCCAGGGGGAGGTGCCGCCCGGCCCGCTGCCCGAGGCCGTGCTCG 385

Qy    246 CTCTTTACAACAGTACCCGCGACCGGCTAGCCGGGGAAAGTGTGCAACCGGAGCCCGAGC 305
      | || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db    386 CCCTGTACAACAGCACCCGCGACCGGCTGGCCGGGGAGAGTGCAGAACCGGAGCCCGAGC 445

Qy    306 CAGAGGCGGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACC 365
      | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db    446 CTGAGGCCGACTACTACGCCAAGGAGGTCACCCGCGTGCTAATGGTGGAAACCCACAACG 505

Qy    366 AAATCTATGATAAAATTCAAGGGCACCCCCACAGCTTATATATGCTGTTCAACACGTCGG 425
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db    506 AAATCTATGACAAGTTCAAGCAGAGTACACACAGCATATATATGTTCTTCAACACATCAG 565

Qy    426 AGCTCCGGGAAGCGGTGCCGGAACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTGCTGA 485
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db    566 AGCTCCGAGAAGCGGTACCTGAACCCGTGTTGCTCTCCCGGGCAGAGCTGCGTCTGCTGA 625

Qy    486 GGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCTT 545
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db    626 GGCTCAAGTTAAAAGTGGAGCAGCACGTGGAGCTGTACCAGAAATACAGCAACAATTCTT 685

Qy    546 GGCGCTACCTCAGCAACCGGCTGC-TGGCCCCCAGTGACTACCGGAGTGGCTGTCTTTT 604
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db    686 GGCGATACCTCAGCAACCGGCTGCTTGGCACCCAGCGACTCGCCAGAGTGGTTATCTTTT 745

Qy    605 GATGTACCCGAGTTGTGCGGCAGTGGCTGACCCGAGAG--GAGGCTATAGAGGGTTTTC 662
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db    746 GATGTACCCGAGTTGTGCGGCAGTGGTTGAGCCGTGGACGGGGAACATTGAGGGCTTTC 805

Qy    663 GCCTCAGTGCCCACTGTTCTCTGTGACAGCAAAGATAAC 700
      ||| || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db    806 GCCTTAGCGCCCACTGCTCCTGTGACAGCAGGGATACC 843
```

RESULT 14
AL530080/c

LOCUS AL530080 841 bp mRNA linear EST 23-MAY-2003

DEFINITION AL530080 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
cDNA clone CS0DD009YM06 3-PRIME, mRNA sequence.

ACCESSION AL530080

VERSION AL530080.2 GI:31067915

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 841)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished

COMMENT On Feb 13, 2001 this sequence version replaced gi:12793573.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
9160.r For more information about this cluster, see

<http://www.genoscope.cns.fr/>

[cgi-bin/cluster.cgi?seq=CS0DD009BG03NP1&cluster=9160.r](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DD009BG03NP1&cluster=9160.r). Contact :

Feng Liang Email : fliang@lifetech.com URL :

<http://fulllength.invitrogen.com/> InVitroGen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DD009BG03NP1.

FEATURES Location/Qualifiers

source

1. .841

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="CS0DD009YM06"

/tissue_type="NEUROBLASTOMA COT 50-NORMALIZED"

/clone_lib="Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

BASE COUNT 150 a 240 c 283 g 153 t 15 others

ORIGIN

Query Match 38.6%; Score 525; DB 9; Length 841;

Best Local Similarity 80.3%; Pred. No. 1.8e-104;

Matches 689; Conservative 8; Mismatches 104; Indels 57; Gaps 5;

Qy 438 CGGTGCCCGGAACCTGTATTGCTCT-CTCGGGCAGAGCTGCGCCTGCTGAGGCTCAAGTTA 496
|||| || |:||| | |||:|||| | ||||| ||||| ||||| |||||

Db 841 CGGTACCTGMACCCTTGTGTCTCCCCGGGCAGAGCTGCTTCTGCTAAGGCTCAAGTTA 782

Qy 497 AAAGTGGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCTGGCGCTACCTC 556
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 781 AAAGTGGAGCAGCACGTGGAGCTGTACCAGAAATACAGCAACAATWCCTGGCGGATACCTC 722

Qy 557 AGCAACCGGCTGCTGGCCCCCAGTGACTACCGGAGTGGCTGTCCTTTGATGTACCGGA 616

```

      |||||:| ||||| ||||| :||| || ||||| | || ||||| |||||:|
Db      721 AGCAACCSGCSGCTGGCACCCAGCSACTCGCCAGAGTGGTTTCTTTGTTGTCACCGKA 662
Qy      617 GTTGTGCGGCAGTGGCTGACCCGCAGAGAGGCTATAGAGGGTTTTTCGCCTCAGTGCCAC 676
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      661 GTTGTGCGGCAGTGGTTGAGCCGTGGAGGGGAAATTAAGG--TTTCGCCTTAGCGCCNAC 604
Qy      677 TGTTCCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAATTCTGGC 736
      | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      603 GGCTCCTGTAAACAGCAGGGATAACACACTGCAAGTGAACATCAACGGGTTAACTACCGGC 544
Qy      737 CGCCGGGTGACCTGGCCACCATTACCGGCATGAACCGGCCCTTCCTGCTCCTCATGGCC 796
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      543 CGCCGAGGTGACCTGGCCACCATTCTTGGCATGAACCGGCCCTTCCTGCTTCTCATGGCC 484
Qy      797 ACCCCGCTGGAGAGGGGCCAGCACCTGCACAGCTCCCGGCACCGCCGAGCCCTGGATACC 856
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      483 ACCCCGCTGGAGAGGGGCCAGCTTCTGCAAAGCTCCCGGCACCGCCGA----- 436
Qy      857 AACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCCTGGATACCAACTACTGC 916
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      435 -----GCCCTGGACACCAACTATTGC 415
Qy      917 TTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGAC 976
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      414 TTCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTGTACATTAACTTCCGCAAGGAC 355
Qy      977 CTGGGCTGGAAGTGGATTTCATGAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCC 1036
      || ||||| ||||| || || ||||| |||||: ||||| ||||| |||||
Db      354 CTCGGCTGGGAGTGGATCCACGAGCCCAAGGGCTWCCATGCCAACTTCTGCCTCGGGCCC 295
Qy      1037 TGTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCTTGCTCTGTACAACCAG 1096
      || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      294 TGCCCTACATTTGGAGCCTGGACACGCAGGACAGCAAGGTCTTGCCCTGTACAACCAG 235
Qy      1097 CACAACCCGGGCGCTCGGCGGCGCCGTGCTGCGTGCCGCAGGCGCTGGAGCCACTGCCC 1156
      || ||||| || || ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      234 CATAACCCGG--GCCTCGGCGGCGCCGTGC-GCGTGCCGCAGGCGCTGGAGCCGCTGCCC 178
Qy      1157 ATCGTGTAATACTACGTGGGCGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGT 1216
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      177 TTCGTGTAATACTACGTGGGCGCAAGCCCAAGGTGGGGCGGCTGTCCAACATGGTTCGTGCGC 118
Qy      1217 TCCTGCAAGTGCAGCTGAGGCCCGCCCCGCCACAGCCCCGCCACCCGGCAGGCCCGG 1276
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      117 TCCTGCAAGGCCGCTGGGGTCCCCGCCCGCCCCGCCCGCCCCGGCAGGCCCGGCC 58
Qy      1277 CCCCACCCCGCCCGCCT 1294
      |||| |||| |||: ||
Db      57 CCCCACCCCGCCCGCCT 40

```

RESULT 15

BI084718/c

LOCUS

BI084718

956 bp

mRNA

linear

EST 20-JUN-2001

DEFINITION

602869722T1 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:5014421 3',
mRNA sequence.

ACCESSION BI084718
 VERSION BI084718.1 GI:14503048
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 956)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: CLONETECH Laboratories, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 <http://image.llnl.gov>
 Plate: LLCM1821 row: 1 column: 06
 High quality sequence start: 3
 High quality sequence stop: 793.
 FEATURES
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5014421"
 /tissue_type="epidermoid carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_102"
 /note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;
 Site_2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Library constructed
 by Ling Hong in the laboratory of Gerald M. Rubin
 (University of California, Berkeley) using ZAP-cDNA
 synthesis kit (Stratagene) and Superscript II RT (Life
 Technologies). Note: this is a NIH_MGC Library."
 BASE COUNT 172 a 273 c 312 g 199 t
 ORIGIN

 Query Match 38.5%; Score 524.6; DB 12; Length 956;
 Best Local Similarity 77.0%; Pred. No. 2.3e-104;
 Matches 757; Conservative 0; Mismatches 159; Indels 67; Gaps 7;

 Qy 329 GAGGTCACCCGCGTGCTAATGGTGGAAAGCGGCAACCAAATCTATGATAAATTCAAGGGC 388
 ||||| | ||| ||||| ||||| | ||| | ||||| |
 Db 955 GAGGTTAACCGGTGCTAAATGGTGGAAACCCACCACGAATCTATGACCAGGTTTCAGCAGA 896

 Qy 389 ACCCCCCACAGCTTATATATGCTGTTCAACACGTC--GGAGCTCCGGGAAGCGGTGCCGG 446
 | | | ||||| ||||| || | ||||| ||||| ||
 Db 895 GTACACACAGCCATAAATATGGTCTTCACACATTTCAGGAGCTTCCGAGAACCGGTACCCT 836

 Qy 447 AACCTGTATTGCTCTCTCGGGCAGAGCTGCGCCTG-----CTGAGGCTCAAGTTAAAAGT 501
 | | || ||| || | || || | | ||||| ||||| |||||

Db 835 GAACCGTGTGGCTCTTCCCGGGGAAGAGCTGCCGTCTGCCTGAGGCTCAAGTTAAAAGT 776
 Qy 502 -GGAGCAGCACGTGGAGCTATACCAGAAATACAGCAATGATTCTTGGCGCTACCTCAGCA 560
 ||| ||||| ||||| ||| | | ||||| ||||| ||||| |||||
 Db 775 GGGACCAGCACGTGGAGCTGTAAACAGGAATACAGCACAATTCTTGGCGATACCTCAGCA 716
 Qy 561 ACCGGCTGCTGGCCCCCAGTGA--CTCACCGGAGTGGCTGTCCTTTGATGTCACCGGAGT 618
 ||||| ||| ||||| || || || ||||| | || ||||| ||||| |||||
 Db 715 ACCGGCTGGTGGCACCCAGCGAACTCGCCAGAGTGGTTATCTTTGATGTCACCGGAGT 656
 Qy 619 TGTGCGGCAGTGGCTGACCCGAG-AGAGGCTATAGAGGGTTTTCGCCCTCAGTGCCCACT 677
 ||||| ||||| ||| ||| | || || || ||||| ||||| ||||| |||||
 Db 655 TGTGCGGCAGTGGTTGAGCCGTGGAAGGGGAAATTGAGGGCTTTTCGCCCTTAGCGCCCACT 596
 Qy 678 GTTCCTGTGACAGCAAAGATAACACACTCCACGTGGAAATTAACGGGTTCAATTCTGGCC 737
 | ||||| ||||| ||||| ||||| || ||||| || ||||| || |||||
 Db 595 GCTCCTGTGACAGCAGGGATAACACACTGCAAGTGGACATCAACGGGTTCACTACCGGCC 536
 Qy 738 GCCGGGGTGACCTGGCCACCATTACGGCATGAACCGGCCCTTCTGCTCCTCATGGCCA 797
 |||| | ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 535 GCCGAGGTGACCTGGCCACCATTATGGCATGAACCGGCCCTTCTGCTTCTCATGGCCA 476
 Qy 798 CCCCCTGGAGAGGGCCAGCACCTGCACAGCTCCCGGCACCGCCGAGCCCTGGATACCA 857
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 475 CCCCCTGGAGAGGGCCAGCATCTGCAAAGCTCCCGGCACCGCCGAGCCCTGGAC---- 420
 Qy 858 ACAGCTACCCATACGACGTGCCAGACTACGCATCTCTGGCCCTGGATACCAACTACTGCT 917
 ||||| ||||| |||||
 Db 419 -----ACCAACTATTGCT 407
 Qy 918 TCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTCTACATTGACTTCCGGAAGGACC 977
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 406 TCAGCTCCACGGAGAAGAACTGCTGCGTGCGGCAGCTGTACATTGACTTCCGGAAGGACC 347
 Qy 978 TGGGCTGGAAGTGATTCATGAACCCAAGGGCTACCATGCCAATTTCTGCCTGGGGCCCT 1037
 | ||||| ||||| || || ||||| ||||| ||||| ||||| ||||| |||||
 Db 346 TCGGCTGGAAGTGATCCACGAGCCCAAGGGCTACCATGCCAATTTCTGCCTCGGGCCCT 287
 Qy 1038 GTCCCTACATCTGGAGCCTAGACACTCAGTACAGCAAGGTCCTGGCTCTGTACAACCAGC 1097
 | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 286 GCCCCTACATTTGGAGCCTGGACACGCAGTACAGCAAGGTCCTGGCCCTGTACAACCAGC 227
 Qy 1098 ACAACCCGGGCGCGTCGGCGGCGCCGTGCTGCGTGCCGCAGGCGCTGGAGCCACTGCCCA 1157
 | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 226 ATAACCCGGGCGCCTCGGCGGCGCCGTGCTGCGTGCCGCAGGCGCTGGAGCCGCTGCCCA 167
 Qy 1158 TCGTGTA TACTACGTGGGCGGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGTT 1217
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 166 TCGTGTA TACTACGTGGGCGGCAAGCCCAAGGTGGAGCAGCTGTCCAACATGATCGTGCGCT 107
 Qy 1218 CCTGCAAGTG CAGCTGAGGCCCCGCCCCGCCACAGCCCCGCCACCCGGCAGGCCCCGGC 1277
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 106 CCTGCAAGTG CAGCTGAGGTCCCGCCCCGCC-----CCGCCCCGCCCGGCAGGCCCCGGC 52
 Qy 1278 CCCACCCCCGCCCCGCTCACC GG 1300
 ||||| ||||| ||| |
 Db 51 CCCACCCCCGCCCCGCCCCCGCTG 29

Search completed: October 28, 2003, 00:08:32
Job time : 3384.39 secs

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OM protein - protein search, using sw model

1902.657 Million cell updates/sec

Sequence: 1 MAPSGRLRLPLLLPLLWLLV.....GRKPKVEQLSNMIVRSCKCS 407

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Maximum DB seg length: 2000000000

Listing first 45 summaries

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24: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	2038.5	94.0	390	23	AAE13596		Porcine transformi
2	1946.5	89.7	390	22	AAM39186		Human polypeptide
3	1939.5	89.4	390	7	AAP61468		PreTGF-beta gene p
4	1939.5	89.4	390	11	AAR04034		Sequence of pre-TG
5	1939.5	89.4	390	11	AAR05258		Human pre-transfor
6	1939.5	89.4	390	12	AAR13813		Human pro-TGF-beta
7	1939.5	89.4	390	16	AAR73596		Human TGF-beta 1 p
8	1939.5	89.4	390	17	AAR90827		Pre-transforming g
9	1936.5	89.3	390	23	AAU77101		Human transforming
10	1936.5	89.3	390	23	AAE16943		Human transforming
11	1936	89.3	391	24	ABB82780		TGFB1 Arg25Pro pol
12	1934.5	89.2	390	13	AAR20124		Sequence of simian
13	1930.5	89.0	390	15	AAR46227		Human pre-TGF-beta
14	1929	88.9	391	16	AAR83054		Transforming growt
15	1928.5	88.9	390	19	AAW78785		Human pre-transfor
16	1927.5	88.9	390	22	AAB84601		Nucleotide sequenc
17	1925	88.8	391	9	AAP81362		Human transforming
18	1924	88.7	434	11	AAR03743		Monkey transformin
19	1920.5	88.5	390	24	ABB82781		TGFB1 Arg25Pro pol
20	1903.5	87.8	386	11	AAR05663		Simian Transformin
21	1898	87.5	387	11	AAR05664		Simian Transformin
22	1887.5	87.0	390	11	AAR05492		Chimeric simian TG
23	1883.5	86.8	390	13	AAR27522		TGF-beta 1/beta 2
24	1864	85.9	389	13	AAR29657		TGF-beta 1. Homo
25	1859	85.7	453	22	AAM40972		Human polypeptide
26	1778.5	82.0	390	13	AAR20126		Sequence of hybrid
27	1777.5	82.0	390	11	AAR05749		Human TGF-Beta2 ex
28	1771.5	81.7	390	11	AAR05665		Human Transforming
29	1769.5	81.6	390	11	AAR05666		Hybrid transformin
30	1762	81.2	391	10	AAP91900		Sequence encoded b
31	1735	80.0	389	16	AAR79921		Simian-human hybri
32	1320	60.9	278	15	AAR53090		Polypeptide cross-
33	1315	60.6	278	12	AAR12541		Latency associated
34	1282.5	59.1	458	23	ABG31507		LAP-mIFNB construc
35	1282.5	59.1	463	23	ABG31510		LAP-huIFNB constru
36	1189	54.8	290	22	ABG06792		Novel human diagno
37	1155	53.3	450	23	ABG31508		mIFNB-LAP construc
38	1138	52.5	448	23	ABG31509		huIFNB-LAP construc
39	944	43.5	227	22	ABG20234		Novel human diagno
40	901	41.5	236	22	ABG20233		Novel human diagno
41	887.5	40.9	382	21	AAB08338		Amino acid sequenc
42	887.5	40.9	382	23	AAU77105		Frog transforming
43	849.5	39.2	456	19	AAW78786		Pig transforming g
44	845.5	39.0	412	16	AAR73598		Human TGF-beta 3 p
45	843	38.9	456	15	AAR46228		Pig TGF-beta-3. S

ALIGNMENTS

RESULT 1

AAE13596

ID AAE13596 standard; Protein; 390 AA.

XX

AC AAE13596;

XX

DT 26-FEB-2002 (first entry)

XX

DE Porcine transforming growth factor beta 1 (TGF-beta1) mutant.

XX

KW Porcine; transforming growth factor beta 1; TGF-beta1; gene therapy;
KW IBD; inflammatory bowel disease; autoimmune disease; immunosuppressive;
KW multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus;
KW diabetes mellitus; sarcoidosis; psoriasis; dermatological; mutant;
KW mutein.

XX

OS Sus scrofa.

XX

FH Key Location/Qualifiers

FT Misc-difference 223

FT /note= "Wild type Cys substituted with Ser"

FT Misc-difference 225

FT /note= "Wild type Cys substituted with Ser"

XX

PN WO200181404-A2.

XX

PD 01-NOV-2001.

XX

PF 20-APR-2001; 2001WO-US12980.

XX

PR 20-APR-2000; 2000US-199014P.

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Strober W, Nakamura K, Kitani A, Fuss IJ;

XX

DR WPI; 2002-026155/03.

DR N-PSDB; AAD22696.

XX

PT Composition for treating autoimmune diseases e.g. inflammatory bowel
PT disease in humans, comprises vector containing transforming growth
PT factor-beta under the control of inducible promoter -

XX

PS Example 1; Fig 1; 78pp; English.

XX

CC The invention relates to a composition containing a vector comprising a
CC gene encoding a regulatory transcription factor under the control of a
CC promoter encoding a transforming growth factor-beta (TGF-beta). The
CC vector is useful for expressing TGF-beta, such as TGF-beta1, TGF-beta2
CC or TGF-beta3, its variants or homologues, by transfecting a cell which
CC is part of a host suspected of having an autoimmune disease, especially
CC inflammatory bowel disease (IBD), under conditions such that the
CC polypeptide encoded by the nucleic acid sequence in the vector is
CC expressed. The vector is delivered using a delivery system. The delivery
CC of the vector results in substantial elimination of symptoms of the
CC autoimmune disease and increased production of IL-10 by the host. The
CC composition is useful for treating various diseases with an autoimmune

CC component such as multiple sclerosis, rheumatoid arthritis, systemic
CC lupus erythematosus, insulin-dependent diabetes mellitus, sarcoidosis
CC and psoriasis, and also for assaying the expression of a gene in a cell.
CC The vector is further useful for screening of the effect of test
CC compounds on cytokine (e.g. TGF-beta) expression of transfected cells.
CC The present sequence is porcine TGF-beta1 mutant.

XX

SQ Sequence 390 AA;

Query Match 94.0%; Score 2038.5; DB 23; Length 390;
Best Local Similarity 95.3%; Pred. No. 1.7e-170;
Matches 388; Conservative 0; Mismatches 2; Indels 17; Gaps 1;

```
Qy      1 MAPSGLRLLPLLLPLLWLLVLTGPRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
      |||
Db      1 MAPSGLRLLPLLLPLLWLLVLTGPRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60

Qy     61 SPPSQGDVPPGGLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
      |||
Db     61 SPPSQGDVPPGGLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120

Qy    121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
      |||
Db    121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180

Qy    181 YLSNRL LAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHCSCDSKDNTLHVEINGFN 240
      |||
Db    181 YLSNRL LAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHSSSDSKDNTLHVEINGFN 240

Qy    241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNSYPYDVPDYASLALDTN 300
      |||
Db    241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRR-----ALDTN 283

Qy    301 YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 360
      |||
Db    284 YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 343

Qy    361 NQHNP GASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
      |||
Db    344 NQHNP GASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
```

RESULT 2

AAM39186

ID AAM39186 standard; Protein; 390 AA.

XX

AC AAM39186;

XX

DT 22-OCT-2001 (first entry)

XX

DE Human polypeptide SEQ ID NO 2331.

XX

KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;

KW leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200153312-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 26-DEC-2000; 2000WO-US34263.
 XX
 PR 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-0552317.
 PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
 XX
 DR WPI; 2001-442253/47.
 DR N-PSDB; AAI58342.
 XX
 PT Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -
 XX
 PS Example 4; SEQ ID NO 2331; 10078pp; English.
 XX
 CC The invention relates to human nucleic acids (AAI57798-AAI61369) and
 CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 XX
 SQ Sequence 390 AA;

Query Match 89.7%; Score 1946.5; DB 22; Length 390;
 Best Local Similarity 90.4%; Pred. No. 2.1e-162;
 Matches 368; Conservative 10; Mismatches 12; Indels 17; Gaps 1;

Qy 1 MAPSGLRLLPLLLPLLWLLVLTTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60

Db	1	MPPSGLRLPLLLPLLWLLVLTTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA	60
Qy	61	SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI	120
Db	61	SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI	120
Qy	121	YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR	180
Db	121	YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNNSWR	180
Qy	181	YLSNRL LAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHCSCDSKDNTLHVEINGFN	240
Db	181	YLSNRL LAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT	240
Qy	241	SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNSYPYDVPDYASIALDTN	300
Db	241	TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR-----ALDTN	283
Qy	301	YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY	360
Db	284	YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY	343
Qy	361	NQHNP GASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS	407
Db	344	NQHNP GASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS	390

RESULT 3

AAP61468

ID AAP61468 standard; Protein; 390 AA.

XX

AC AAP61468;

XX

DT 31-OCT-2002 (updated)

DT 28-OCT-1991 (first entry)

XX

DE PreTGF-beta gene product.

XX

KW Transforming growth factor beta; cancer; wound healing.

XX

OS Unidentified.

XX

FH Key Location/Qualifiers

FT Protein 279..390

XX

PN EP200341-A.

XX

PD 10-DEC-1986.

XX

PF 21-MAR-1986; 86EP-0302112.

XX

PR 22-MAR-1985; 85US-0715142.

PR 13-MAR-1987; 87US-0025423.

XX

PA (GETH) GENENTECH INC.

XX

PI Derynck RMA;
 XX
 DR WPI; 1986-326875/50.
 DR N-PSDB; AAN60972.
 XX
 PT TGF-beta prodn. from transformed hosts - useful esp. for treating
 PT wounds (J6 2/9/86).
 XX
 PS Disclosure; Fig 1b; 26pp; English.
 XX
 CC The gene product is known to stimulate cell proliferation and
 CC inhibit anchorage-dependent growth of a variety of human cancer cell
 CC lines, it is esp. useful in treatment of burns and the promotion of
 CC surface and internal wound healing. TGF-beta may be expressed from a
 CC transformed CHO cell line.
 CC (Updated on 31-OCT-2002 to add missing OS field.)
 XX
 SQ Sequence 390 AA;

Query Match 89.4%; Score 1939.5; DB 7; Length 390;
 Best Local Similarity 90.2%; Pred. No. 8.5e-162;
 Matches 367; Conservative 10; Mismatches 13; Indels 17; Gaps 1;

Qy	1	MAPSGRLRLPLLLPLLWLLVLTGPRPAAGLSTCKTIDMELVKKRIE	AIRGQILSKLRLA	60
Db	1	MPPSGRLRLPLLLPLLWLLVLTGPPAAGLSTCKTIDMELVKKRIE	AIRGQILSKLRLA	60
Qy	61	SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEV	TRVLMVESGNQI	120
		:		
Db	61	SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEV	TRVLMVETHNEI	120
Qy	121	YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR		180
		: :		
Db	121	YDKFKQSTHSIYMFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNNSWR		180
Qy	181	YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHCSCDSKDNTLHVEINGFN		240
		:		
Db	181	YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT		240
Qy	241	SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNSYPYDVPDYASLALDTN		300
		:		
Db	241	TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR-----ALDTN		283
Qy	301	YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY		360
Db	284	YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY		343
Qy	361	NQHNPASAAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS		407
Db	344	NQHNPASAAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS		390

RESULT 4
 AAR04034
 ID AAR04034 standard; protein; 390 AA.
 XX
 AC AAR04034;

```

XX      DT      25-MAR-2003      (updated)
XX      DT      31-OCT-2002      (updated)
XX      DT      31-MAY-1989      (first entry)
XX
DE      Sequence of pre-TGF-beta 1.
XX
KW      Transforming growth factor beta-3 (TGF beta 3); tumour cells; growth
KW      inhibition.
XX
OS      Homo sapiens.
XX
FH      Key              Location/Qualifiers
FT      CDS              348..500
XX
PN      WO8912101-A.
XX
PD      14-DEC-1989.
XX
PF      08-JUN-1988;      88WO-US01945.
XX
PR      08-JUN-1988;      88WO-US01945.
XX
PA      (GETH ) GENENTECH INC.
XX
PI      Dernyck RMA,  Goeddel DV;
XX
DR      WPI; 1990-007474/01.
DR      N-PSDB; AAQ02815.
XX
PT      Nucleotide sequence encoding transforming growth factor beta-3 used as a
PT      probe, or to produce TGF beta 3, for inhibiting growth of certain normal
PT      and neoplastic cells, eg A549.
XX
PS      Disclosure; Fig. 2; 61pp; English.
XX
CC      Sequence is an exon of transforming growth factor-beta 1 (pre-TGF-beta
CC      1) polypeptide and corresponds to AA's 288-338 of mature TGF-beta 1. The
CC      nucleic acid encoding second subtype of TGF-beta (TGF-beta 3) is useful
CC      as a probe or to produce TGF-beta 3 for inhibition of normal and
CC      neoplastic cell growth.
CC      (Updated on 31-OCT-2002 to add missing OS field.)
CC      (Updated on 25-MAR-2003 to correct PR field.)
CC      (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ      Sequence      390 AA;

Query Match      89.4%;  Score 1939.5;  DB 11;  Length 390;
Best Local Similarity  90.2%;  Pred. No. 8.5e-162;
Matches 367;  Conservative 10;  Mismatches 13;  Indels 17;  Gaps 1;

Qy      1  MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
      |  |||||
Db      1  MPPSGLRLLPLLLPLLWLLVLTPGPPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
      |  |||||

Qy      61  SPSPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
      |||||:|||||

```

[illegible]

RESULT 5

ID AAR05258 standard; protein; 390 AA.

XX

AC AAR05258;

XX

DT 25-MAR-2003 (updated)

DT 05-AUG-1990 (first entry)

XX

DE Human pre-transforming growth factor-beta-1 (pre-TGF-beta-1).

XX

KW Transforming growth factor-beta-1 (TGF-beta-1);

KW neoplastic cell line inhibition;

KW EGF-potentiated anchorage-independent growth.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT Peptide 1..278

FT	Protein	279..2011
----	---------	-----------

FT Domain 8..23

```
FT                               /note="hydrophobic domain"
```

FT	Modified-site	82..84
----	---------------	--------

FT /note="potential N-glycosylation site "

FT Modified-site 136..138

FT /note="as above"

FT Modified-site 176..178

FT /note="as above"

FT Cleavage-site 277..278

FT /note="proteolytic cleavage site"

XX

PN US4886747-A.

XX

PD 12-DEC-1989.

Qy 361 NQHNP GASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 344 NQHNP GASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390

RESULT 6

AAR13813

ID AAR13813 standard; Protein; 390 AA.

XX

AC AAR13813;

XX

DT 20-NOV-1991 (first entry)

XX

DE Human pro-TGF-beta 1.

XX

KW Osteogenetic; tumoricidal.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT	Peptide	1..29
----	---------	-------

FT		/note= "signal peptide"
----	--	-------------------------

FT	Peptide	30..390
----	---------	---------

FT		/note= "pro-TGF-beta 1"
----	--	-------------------------

FT	Peptide	279..390
----	---------	----------

FT		/note= "TGF-beta 1"
----	--	---------------------

XX

PN JP03180192-A.

XX

PD 06-AUG-1991.

XX

PF 07-DEC-1989; 89JP-0318243.

XX

PR 07-DEC-1989; 89JP-0318243.

XX

PA (KIRI) KIRIN BREWERY KK.

XX

DR WPI; 1991-271579/37.

DR N-PSDB; AAQ13392.

XX

PT Human pro-TGF-beta 1 prodn., for osteo-genetic activity - by

PT preparing DNA chain contg. base sequence coding for human

PT pre:pro-TGF-beta 1, forming expression vector etc.

XX

PS Claim 1; Fig 1; 16pp; Japanese.

XX

CC The amino acid sequence codes for human prepro-TGF-beta 1 which

CC can be produced by recombinant methods, it has osteogenetic and

CC tumoricidal activity.

XX

SQ Sequence 390 AA;

Query Match 89.4%; Score 1939.5; DB 12; Length 390;

Best Local Similarity 90.2%; Pred. No. 8.5e-162;

Matches 367; Conservative 10; Mismatches 13; Indels 17; Gaps 1;

Qy	1	MAPSGLRLLPLLLPLLWLLVLTGPRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKRLA	60
Db	1	MPPSGLRLLPLLLPLLWLLVLTGPPPAAGLSTCKTIDMELVKRKRIEAIRGQILSKRLA	60
Qy	61	SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI	120
Db	61	SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI	120
Qy	121	YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR	180
Db	121	YDKFKQSTHSIYMFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNNSWR	180
Qy	181	YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAI EGFRLSAHCSCDSKDNTLHVEINGFN	240
Db	181	YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEI EGFRLSAHCSCDSRDNTLQVDINGFT	240
Qy	241	SGRRGDLATI HGMNRPFLLL MATPLERAQHLHSSRHRRALDTNSYPYDVPDYASLALDTN	300
Db	241	TGRRGDLATI HGMNRPFLLL MATPLERAQHLQSSRHRR-----ALDTN	283
Qy	301	YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY	360
Db	284	YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY	343
Qy	361	NQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS	407
Db	344	NQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS	390

AAR73596

XX

XX

DT 20-DEC-1995 (first entry)

DE Human TGF-beta 1 protein.

KW Transforming growth factor-beta; Human TGF-beta protein; TGF-beta 1;

KW bone-inducing cofactor.

OS Homo sapiens.

PN US5409896-A.

PD 25-APR-1995.

PF 12-NOV-1993; 93US-0132405.

PR 01-SEP-1989; 89US-0401906.

PR 18-MAY-1993; 93US-0063841.

XX

RESULT 8

AAR90827

ID AAR90827 standard; Protein; 390 AA.

XX

AC AAR90827;

XX

DT 25-MAR-2003 (updated)

DT 25-JAN-1980 (first entry)

XX

DE Pre-transforming growth factor beta 1.

XX

KW transforming growth factor beta 1; wound healing;

KW recombinant production.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT	Domain	8..23
----	--------	-------

FT		/note= "hydrophobic domain"
----	--	-----------------------------

FT	Modified-site	82..84
----	---------------	--------

FT		/note= "potential N-glycosylation site"
----	--	-----------------------------------------

FT	Modified-site	136..138
----	---------------	----------

FT		/note= "potential N-glycosylation site"
----	--	-----------------------------------------

FT	Modified-site	176..178
----	---------------	----------

FT		/note= "potential N-glycosylation site"
----	--	-----------------------------------------

FT	Cleavage-site	277..279
----	---------------	----------

FT		/note= "trypsin-like peptidase cleavage site"
----	--	-----------------------------------------------

FT	Protein	279..390
----	---------	----------

FT		/label= mature_TGF_beta_1
----	--	---------------------------

XX

PN US5482851-A.

XX

PD 09-JAN-1996.

XX

PF 05-NOV-1993; 93US-0147364.

XX

PR 13-MAR-1987; 87US-0025423.

PR 22-MAR-1985; 85US-0715142.

PR 04-AUG-1989; 89US-0389929.

PR 04-MAR-1992; 92US-0845893.

PR 05-NOV-1993; 93US-0147364.

XX

PA (GETH) GENENTECH INC.

XX

PI Derynck RMA, Goeddel DV;

XX

DR WPI; 1996-076891/08.

DR N-PSDB; AAT15720.

XX

PT New recombinant human transforming growth factor-beta prods. - produced

PT using Chinese hamster ovary cells, for use in diagnostic applications

PT or in therapy

XX

PS Example 3; Fig 1A-C; 26pp; English.

XX

CC The pre-transforming growth factor (TGF) beta 1 protein is encoded
CC by AAT15720. The mature TGF beta 1 monomer is cleaved from the
CC precursor at the Arg-Arg dipeptide immediately preceding the mature
CC TGF-beta 1 NH2-terminus. It does not contain a recognisable N-terminal
CC signal peptide typical of most secreted proteins. The pre-TGF beta 1
CC contains several pairs of basic residues which could undergo
CC post-translational cleavage and give rise to separate polypeptide
CC entities. The precursor contains 3 potential N-glycosylation sites, none
CC of which are localised in the mature TGF beta 1. This is useful in
CC purification of the mature protein. TGF beta 1 can be used in, e.g. wound
CC healing.

XX

Query Match 89.4%; Score 1939.5; DB 17; Length 390;
Best Local Similarity 90.2%; Pred. No. 8.5e-162;
Matches 367; Conservative 10; Mismatches 13; Indels 17; Gaps 1;

QY 61 SPSPQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
| | | | | : | | | | | | | | | | | | | | | | | | | | : | : |

Qy 121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
| | | | : | : | | | | | | | | | | | | | | | | | | | : | |

Qy 181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAI EGFRLSAHCSCDSKDNLT LHEINGFN 240
 | | | | | | | | | | : | | | | | | | | | | : | | | | : | | |

QY 241 SGRRGDLATIHGMNRPFLLLMTPLERAQHLHSSRRHRRALDTNSYPYDVPDYASLALDTN 300
: |||||

Qy 301 YCFSSSTEKNCCVRQLYIDFRKDLGWKIHEPKGYHANFCLGPCPYIWSLDTQYSKVLLAY 360
 |
 |

Qy 361 NQHNP GASAAPCCVPQALEPLPIVYVYVGRKPKVEQLSNMIVRSCKCS 407

RESULT 9

XX
 KW Human; transforming growth factor beta; TGF-beta; insulin production;
 KW type I diabetes mellitus; pancreatic cell outgrowth; wound healing;
 KW pancreatic duct tissue; ischaemia; stroke; nervous system aging;
 KW neurological condition; neurodegenerative disease; inflammation;
 KW vasal injury; chemical injury; traumatic injury; tumour-induced injury;
 KW amyotrophic lateral sclerosis; spinocerebellar degeneration;
 KW immunological disease; multiple sclerosis; TGF-beta-1.
 XX
 OS Homo sapiens.
 XX
 PN WO200212336-A2.
 XX
 PD 14-FEB-2002.
 XX
 PF 09-FEB-2001; 2001WO-US04192.
 XX
 PR 09-AUG-2000; 2000US-0635368.
 XX
 PA (CURI-) CURIS INC.
 XX
 PI Wang M, Pang K;
 XX
 DR WPI; 2002-257468/30.
 XX
 PT Treating a subject with a disorder resulting from insufficient insulin
 PT production, and inducing outgrowth of pancreatic cells, involves using
 PT a transforming growth factor beta therapeutic -
 XX
 PS Disclosure; Fig 1; 77pp; English.
 XX
 CC The invention relates to treating a subject with a disorder resulting
 CC from insufficient insulin production, involving contacting the subject
 CC with a transforming growth factor beta (TGF-beta) therapeutic. TGF-beta
 CC polypeptides can be used for treating a subject with a disorder resulting
 CC from insufficient insulin production, e.g. type I diabetes mellitus, and
 CC for inducing outgrowth of pancreatic cells associated with pancreatic
 CC duct tissue within a subject. A composition comprising a TGF-beta protein
 CC may be useful in wound healing and treatment of neurological conditions
 CC derived from acute, subacute or chronic injury to the nervous system,
 CC including traumatic injury, chemical injury, vasal injury and deficits
 CC (such as ischaemia resulting from stroke), together with
 CC infectious/inflammatory and tumour-induced injury, aging of the nervous
 CC system including Alzheimer's disease, chronic neurodegenerative diseases
 CC including Parkinson's disease, Huntington's chorea, amyotrophic lateral
 CC sclerosis, spinocerebellar degenerations and chronic immunological
 CC diseases of the nervous system or affecting the nervous system, including
 CC multiple sclerosis. This sequence represents the human TGF-beta-1
 CC protein.
 XX
 SQ Sequence 390 AA;

Query Match 89.3%; Score 1936.5; DB 23; Length 390;
 Best Local Similarity 90.2%; Pred. No. 1.6e-161;
 Matches 367; Conservative 10; Mismatches 13; Indels 17; Gaps 1;

Qy 1 MAPSGLRLLPLLLPLLWLLVLTTPGRPAAGLSTCKTIDMELVKRKRIEAI RGQILSKLRLA 60

Db	1	MPPSGLRLLLLLLPLLWLLVLTGPRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKRLA	60
QY	61	SPPSQGDVPPGGLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI	120
Db	61	SPPSQGEVPPGGLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI	120
QY	121	YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR	180
Db	121	YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNNSWR	180
QY	181	YLSNRL LAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHCSCDSKDNTLHVEINGFN	240
Db	181	YLSNRL LAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT	240
QY	241	SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNSYPYDVPDYASIALDTN	300
Db	241	TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR-----ALDTN	283
QY	301	YCFSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY	360
Db	284	YCFSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY	343
QY	361	NQHNP GASAAPCCVPQALEPLPIVYVGRKPKVEQLSNMIVRSCKCS	407
Db	344	NQHNP GASAAPCCVPQALEPLPIVYVGRKPKVEQLSNMIVRSCKCS	390

RESULT 10

AAE16943

ID AAE16943 standard; Protein; 390 AA.

XX

AC AAE16943;

XX

DT 18-APR-2002 (first entry)

XX

DE Human transforming growth factor-beta1 (TGF-beta1) protein.

XX

KW Human; transforming growth factor-beta1; TGF-beta1; osteoporosis;
 KW latency associated peptide; LAP; integrin alphavbeta3; apoptosis;
 KW immunomodulation; inflammatory disease; fibrotic disease; cancer;
 KW diabetic retinopathy; chronic obstructive pulmonary disorder;
 KW bone resorption; rheumatoid arthritis; psoriasis; restenosis;
 KW atherosclerosis; liver fibrosis; asthma; cytostatic; osteopathic;
 KW ophthalmological; antiarteriosclerotic; vasotropic.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 1..29

FT /label= Signal_peptide

FT Region 30..278

FT /note= "LAP-beta1"

FT Domain 244..246

FT /note= "RGD motif"

FT Protein 279..390

FT /note= "Human mature TGF-beta1 protein"


```

Db      121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKVKVEQHVELYQKYSNNSWR 180
QY      181 YLSNRL LAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHCSCDSKDNTLHVEINGFN 240
        |||
Db      181 YLSNRL LAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT 240
        |||
QY      241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNSYPYDVPDYASLALDTN 300
        :|||
Db      241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR-----ALDTN 283
        |||
QY      301 YCFSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 360
        |||
Db      284 YCFSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 343
        |||
QY      361 NQHNP GASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
        |||
Db      344 NQHNP GASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
        |||

```

RESULT 11

ABB82780

ID ABB82780 standard; Protein; 391 AA.

XX

AC ABB82780;

XX

DT 18-MAR-2003 (first entry)

XX

DE TGFB1 Arg25Pro polymorphism G-allele protein sequence.

XX

KW Polymorphism; transforming growth factor beta 1; TGFB1; TGFbeta-1;

KW renal failure; nephrotropic; human; allele.

XX

OS Homo sapiens.

XX

PN WO200290585-A2.

XX

PD 14-NOV-2002.

XX

PF 08-MAY-2002; 2002WO-GB02066.

XX

PR 09-MAY-2001; 2001GB-0011277.

XX

PA (UYSH-) UNIV SHEFFIELD HALLAM.

XX

PI El-Nahas AM, Blakemore A, Khalil MS;

XX

DR WPI; 2003-120560/11.

DR N-PSDB; ABV75391.

XX

PT Determining an individual's susceptibility to the progression of renal

PT failure comprises detecting the presence of a genetic polymorphism

PT pattern in transforming growth factor beta 1 (TGFB1) gene in a sample

PT from the individual -

XX

PS Claim 51; Page 59-61; 62pp; English.

XX

CC The invention relates to determining an individual's susceptibility to

DE Sequence of simian transforming growth factor (TGF) beta-1.
 XX
 KW Hypertension therapy; hypotensive agent; blood pressure modulator.
 XX
 OS Monkey.
 XX
 FH Key Location/Qualifiers
 FT Peptide 8..21
 FT Protein 279..390
 XX
 PN WO9119513-A.
 XX
 PD 26-DEC-1991.
 XX
 PF 20-JUN-1991; 91WO-US04449.
 XX
 PR 20-JUN-1990; 90US-0541221.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Oleson FB, Comerreski CR;
 XX
 DR WPI; 1992-024199/03.
 DR N-PSDB; AAQ20289.
 XX
 PT Use of transforming growth factor (TGF)-beta and their
 PT antagonists - for modulating blood pressure, for treating
 PT hypertension and hypotension
 XX
 PS Disclosure; Fig 1; 42pp; English.
 XX
 CC A new method for treating hypertension comprises administering a
 CC transforming growth factor (TGF)-beta to an individual at a dose
 CC effective for lowering blood pressure; the TGF-beta may be e.g.
 CC mature TGF-beta, TGF-beta2, a mature TGF-beta1/beta2 hybrid, TGF-
 CC beta1 precursor, a latent TGF-beta2 precursor, hybrid TGF-beta1/TGF-
 CC beta2 precursor, a latent TGF-beta1 complex or a latent TGF-beta2
 CC complex.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 390 AA;

Query Match 89.2%; Score 1934.5; DB 13; Length 390;
 Best Local Similarity 89.9%; Pred. No. 2.3e-161;
 Matches 366; Conservative 10; Mismatches 14; Indels 17; Gaps 1;

```

QY      1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1 MPPSGLRLLPLLLPLLWLLVLTPSRPAAGLSTCKTIDMELVKRKRIETIRGQILSKLRLA 60

QY     61 SPSPQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
      | | | | | : | | | | | | | | | | | | | | | | | | | | | | | | : | : |
Db     61 SPSPQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120

QY    121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
      | | | | : | : | | | | | | | | | | | | | | | | | | | | : | | |
Db    121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNNSWR 180

```

```

Qy      181 YLSNRL LAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHCSCDSKDNTLHVEINGFN 240
      |||:|||||:| |||:|||||
Db      181 YLSNRL LAPSNSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSKDNTLQVDINGFT 240

Qy      241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTSYYPYDVPDYASLALDTN 300
      :||||| |||
Db      241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR-----ALDTN 283

Qy      301 YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 360
      |||:|||||:| |||:|||||:| |||:|||||:| |||:|||||
Db      284 YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 343

Qy      361 NQHNP GASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
      |||:|||||:| |||:|||||:| |||:|||||:| |||:|||||
Db      344 NQHNP GASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390

```

RESULT 13

AAR46227

ID AAR46227 standard; Protein; 390 AA.

XX

AC AAR46227;

XX

DT 25-MAR-2003 (updated)

DT 09-JUL-1994 (first entry)

XX

DE Human pre-TGF-beta-1.

XX

KW TGF-beta-1; TGF-beta-2; transforming growth factor beta-1;

KW transforming growth factor beta-3; recombinant; wound healing;

KW vulnerary.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 279..390

FT /label= Mat_peptide

FT Cleavage-site 279

FT /note= "TGF-beta-1 release site"

FT Modified-site 82..84

FT /label= N-glycosylation_site

FT Modified-site 136..138

FT /label= N-glycosylation_site

FT Modified-site 176..178

FT /label= N-glycosylation_site

XX

PN US5284763-A.

XX

PD 08-FEB-1994.

XX

PF 04-MAR-1992; 92US-0845893.

XX

PR 22-MAR-1985; 85US-0715142.

PR 13-MAR-1987; 87US-0025423.

PR 04-AUG-1989; 89US-0389929.

PR 04-MAR-1992; 92US-0845893.

XX
PA (GETH) GENENTECH INC.
XX
PI Derynk RMA, Goeddel DV;
XX
DR WPI; 1994-056343/07.
DR N-PSDB; AAQ56923.
XX
PT Nucleic acid sequences encoding transforming growth factor-beta -
PT diagnostic probes, and for use in therapeutics
XX
PS Disclosure; Fig 1b; 25pp; English.
XX
CC cDNA sequences were determined for human pre-TGF-beta-1 (AAQ56923),
CC pig TGF-beta-3 (AAQ56925) and human TGF-beta-3 (AAQ56926), and the
CC corresponding amino acid sequences were determined (AAR46227-29,
CC respectively). A genomic fragment corresponding to a human TGF-
CC beta-1 exon (AAQ56924) was also isolated and its amino acid sequence
CC determined (AAR46230). The sequences have been used in the
CC construction of vectors for the expression of recombinant TGF-
CC beta.
CC (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 390 AA;

Query Match 89.0%; Score 1930.5; DB 15; Length 390;
Best Local Similarity 89.9%; Pred. No. 5.2e-161;
Matches 366; Conservative 10; Mismatches 14; Indels 17; Gaps 1;

QY	1	MAPSGRLRLPLLLPLLWLLVLTGPRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA	60
Db	1	MPPSGRLRLPLLLPLLWLLVLTGPPPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA	60
QY	61	SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI	120
		:	
Db	61	SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEREPEPEADYYAKEVTRVLMVETHNEI	120
QY	121	YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR	180
		: :	
Db	121	YDKFKQSTHSIYMFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNNSWR	180
QY	181	YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHCSCDSKDNTLHVEINGFN	240
Db	181	YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT	240
QY	241	SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRRHRALDTNSYPYDVPDYASLALDTN	300
		:	
Db	241	TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRRHR-----ALDTN	283
QY	301	YCFSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY	360
Db	284	YCFSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY	343
QY	361	NQHNP GASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS	407
Db	344	NQHNP GASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS	390

RESULT 14

AAR83054

ID AAR83054 standard; Protein; 391 AA.

XX

AC AAR83054;

XX

DT 25-JUN-1996 (first entry)

XX

DE Transforming growth factor-beta 1.

XX

KW macrophage inducible nitric oxide synthase; iNOS; constitutive NOS;

KW interleukin-1-beta; transforming growth factor-beta; TGF-beta; IL1-beta;

KW nitric oxide production; hypotension; inflammation; septic shock;

KW treatment.

XX

OS Mammalian sp.

XX

FH Key Location/Qualifiers

FT Protein 279..391

FT /note= "represents the mature active TGF beta-1 mol."

XX

PN W09526745-A1.

XX

PD 12-OCT-1995.

XX

PF 05-APR-1994; 94WO-US03705.

XX

PR 05-APR-1994; 94WO-US03705.

XX

PA (HARD) HARVARD COLLEGE.

XX

PI Lee M, Perrella MA;

XX

DR WPI; 1995-358443/46.

DR N-PSDB; AAT05876.

XX

PT Treatment of hypotension, esp. in septic shock - by administering

PT transforming growth factor-beta e.g. to inhibit inducible nitric

PT oxide synthase gene transcription

XX

PS Disclosure; Fig 17; 52pp; English.

XX

CC Transforming growth factor-beta 1 (TGF-beta 1) has been found to inhibit

CC inducible nitric oxide synthase (iNOS) gene transcription, esp. in

CC interleukin-1-beta (IL1-beta) stimulated rat smooth muscle cells, and at

CC a dose which does not inhibit constitutive NOS. TGF-beta 1 or 2

CC (AAR83055) or their active fragments (esp. derived from the

CC carboxy-terminal 112 amino acids), can be used in the treatment of

CC hypotension, such as that associated with severe inflammation or septic

CC shock.

XX

SQ Sequence 391 AA;

Query Match 88.9%; Score 1929; DB 16; Length 391;

Best Local Similarity 90.0%; Pred. No. 7.1e-161;

Matches 367; Conservative 10; Mismatches 13; Indels 18; Gaps 2;


```

FT      /note= "cleavage site for release of TGF-beta 1"
XX
PN      US5801231-A.
XX
PD      01-SEP-1998.
XX
PF      30-MAY-1995;    95US-0454468.
XX
PR      13-MAR-1987;    87US-0025423.
PR      22-MAR-1985;    85US-0715142.
PR      04-AUG-1989;    89US-0389929.
PR      04-MAR-1992;    92US-0845893.
PR      05-NOV-1993;    93US-0147364.
PR      30-MAY-1995;    95US-0454468.
XX
PA      (GETH ) GENENTECH INC.
XX
PI      Derynck RMA,  Goedel DV;
XX
DR      WPI; 1998-494840/42.
DR      N-PSDB; AAV52933.
XX
PT      DNA encoding transforming growth factor-beta precursor sequence -
PT      useful for analysis to perform manipulations to increase yield of
PT      recombinant production of the protein
XX
PS      Example 3; Fig 1B 1-3; 26pp; English.
XX
CC      This is the amino acid sequence of human transforming growth
CC      factor-beta 1 precursor (preTGF-beta 1). It was deduced from
CC      a preTGF-beta 1 cDNA sequence (see AAV52933). The invention relates
CC      to the recombinant production of TGF-beta. Biologically active
CC      TGF-beta is defined as being capable of inducing EGF-potentiated
CC      anchorage independent growth of target cell lines and/or growth
CC      inhibition of neoplastic cell lines. Nucleic acids encoding
CC      TGF-beta have been isolated and cloned into vectors which are
CC      replicated in bacteria and expressed in eukaryotic cells. TGF-beta
CC      recovered from transformed cells is used in known therapeutic
CC      applications.
CC      (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ      Sequence    390 AA;

Query Match          88.9%;  Score 1928.5;  DB 19;  Length 390;
Best Local Similarity 89.7%;  Pred. No. 7.9e-161;
Matches 365;  Conservative 10;  Mismatches 15;  Indels 17;  Gaps 1;

Qy      1  MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA  60
      |  |||||||||||||||||  ||  |||||||||||  |||||||||||
Db      1  MPPSGLRLLPLLLPLLWLLVLTPGPPAPGLSTCKTIDMEQVKRKRIEAIRGQILSKLRLA  60

Qy      61  SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|:|
Db      61  SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120

Qy      121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
      ||||  :  ||:|  |||||||||||||||||||||||||||||:|

```

```

Db      121 YDKFKQSTHSIYMFNTSELREAVPEPVLLSRAELRLLRLKLVKVEQHVELYQKYSNNSWR 180
Qy      181 YLSNRL LAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHCSCDSKDNTLHVEINGFN 240
        |||
Db      181 YLSNRL LAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT 240
        |||
Qy      241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNSYPYDVPDYASLALDTN 300
        :|||
Db      241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR-----ALDTN 283
        |||
Qy      301 YCFSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 360
        |||
Db      284 YCFSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 343
        |||
Qy      361 NQHNP GASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
        |||
Db      344 NQHNP GASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
        |||

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Search completed: October 28, 2003, 09:06:49
Job time : 34.9534 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 28, 2003, 09:09:54 ; Search time 24.6934 Seconds
(without alignments)
2760.110 Million cell updates/sec

Title: US-10-017-372E-39
Perfect score: 2169
Sequence: 1 MAPSGLRLLPLLLPLLWLLV.....GRKPKVEQLSNMIVRSCKCS 407

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 629382 seqs, 167460630 residues

Total number of hits satisfying chosen parameters: 629382

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	2050.5	94.5	390	11	US-09-214-592-26	Sequence 26, Appl	
2	1949.5	89.9	390	11	US-09-214-592-29	Sequence 29, Appl	
3	1946.5	89.7	390	15	US-10-087-268-2	Sequence 2, Appli	
4	1939.5	89.4	390	15	US-10-087-268-5	Sequence 5, Appli	
5	1936.5	89.3	390	12	US-10-276-947-1	Sequence 1, Appli	
6	1934.5	89.2	390	11	US-09-214-592-33	Sequence 33, Appl	
7	1929	88.9	391	11	US-09-214-592-17	Sequence 17, Appl	
8	1925.5	88.8	390	10	US-09-756-283A-23	Sequence 23, Appl	
9	1913.5	88.2	390	11	US-09-214-592-28	Sequence 28, Appl	
10	1855.5	85.5	390	11	US-09-214-592-20	Sequence 20, Appl	
11	1855.5	85.5	390	11	US-09-214-592-23	Sequence 23, Appl	
12	1592.5	73.4	315	11	US-09-214-592-25	Sequence 25, Appl	
13	1282.5	59.1	455	10	US-09-756-283A-20	Sequence 20, Appl	
14	1159	53.4	447	10	US-09-756-283A-22	Sequence 22, Appl	
15	1067	49.2	373	11	US-09-214-592-32	Sequence 32, Appl	
16	888.5	41.0	412	11	US-09-214-592-31	Sequence 31, Appl	
17	887.5	40.9	382	11	US-09-214-592-34	Sequence 34, Appl	
18	887	40.9	383	10	US-09-756-283A-27	Sequence 27, Appl	
19	851	39.2	409	11	US-09-214-592-27	Sequence 27, Appl	
20	844.5	38.9	410	11	US-09-214-592-22	Sequence 22, Appl	
21	844	38.9	414	11	US-09-214-592-21	Sequence 21, Appl	
22	843.5	38.9	412	11	US-09-214-592-24	Sequence 24, Appl	
23	841.5	38.8	412	11	US-09-214-592-19	Sequence 19, Appl	
24	841.5	38.8	412	14	US-10-028-158-21	Sequence 21, Appl	
25	837.5	38.6	412	10	US-09-756-283A-25	Sequence 25, Appl	
26	829	38.2	414	10	US-09-756-283A-24	Sequence 24, Appl	
27	829	38.2	414	11	US-09-214-592-18	Sequence 18, Appl	
28	825	38.0	412	11	US-09-214-592-30	Sequence 30, Appl	
29	812	37.4	304	10	US-09-756-283A-26	Sequence 26, Appl	
30	753.5	34.7	139	14	US-10-002-278-8	Sequence 8, Appli	
31	638	29.4	112	10	US-09-813-271B-2	Sequence 2, Appli	
32	638	29.4	113	10	US-09-813-398-13	Sequence 13, Appl	
33	638	29.4	114	10	US-09-813-459-22	Sequence 22, Appl	
34	638	29.4	114	14	US-10-115-406-21	Sequence 21, Appl	
35	638	29.4	114	15	US-10-154-333-23	Sequence 23, Appl	

36	638	29.4	115	10	US-09-859-211-47	Sequence 47, Appl
37	638	29.4	115	10	US-09-880-708-25	Sequence 25, Appl
38	638	29.4	115	11	US-09-872-856-47	Sequence 47, Appl
39	638	29.4	115	15	US-10-335-483-29	Sequence 29, Appl
40	562	25.9	98	12	US-10-187-394-1	Sequence 1, Appli
41	542	25.0	116	14	US-10-115-406-24	Sequence 24, Appl
42	542	25.0	116	15	US-10-154-333-26	Sequence 26, Appl
43	535	24.7	112	10	US-09-813-271B-8	Sequence 8, Appli
44	504	23.2	112	10	US-09-813-271B-12	Sequence 12, Appl
45	504	23.2	114	14	US-10-115-406-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1

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US-09-214-592-26
; Sequence 26, Application US/09214592A
; Publication No. US20030027218A1
; GENERAL INFORMATION:
; APPLICANT: Yamasaki,CMotoo
; APPLICANT: Shibata,CKenji
; APPLICANT: Sato,CYasufumi
; TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND
METHOD
; TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS
; FILE REFERENCE: 11060
; CURRENT APPLICATION NUMBER: US/09/214,592A
; CURRENT FILING DATE: 1999-01-18
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE:
; SEQ ID NO 26
; LENGTH: 390
; TYPE: PRT
; ORGANISM: porcine
US-09-214-592-26

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Query Match 94.5%; Score 2050.5; DB 11; Length 390;
Best Local Similarity 95.3%; Pred. No. 7.2e-183;
Matches 388; Conservative 1; Mismatches 1; Indels 17; Gaps 1;

Qy	1	MAPSGRLRLPLLLPLLWLLVLTTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA	60
Db	1	MPPSGLRLLPLLLPLLWLLVLTTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA	60
Qy	61	SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI	120
Db	61	SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMLESQI	120
Qy	121	YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR	180
Db	121	YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR	180
Qy	181	YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAI EGFRLSAHCSCDSKNTLHVEINGFN	240
Db	181	YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAI EGFRLSAHCSCDSKNTLHVEINGFN	240

[illegible]

RESULT 2

US-09-214-592-29

; Sequence 29, Application US/09214592A

; Publication No. US20030027218A1

; GENERAL INFORMATION:

; APPLICANT: Yamasaki, CMotoo

APPLICANT: Shibata, CKenji

; APPLICANT: Sato, CYasufumi

TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND
 METHOD

; TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS

FILE REFERENCE: 11060

CURRENT APPLICATION NUMBER: US/09/214,592A

CURRENT FILING DATE: 1999-01-18

NUMBER OF SEQ ID NOS: 34

; SOFTWARE:

SEQ ID NO 29

LENGTH: 390

; TYPE: PRT

ORGANISM: ovine

US-09-214-592-29

Query Match 89.9%; Score 1949.5; DB 11; Length 390;

Best Local Similarity 90.2%; Pred. No. 1.9e-173;

Matches 367; Conservative 10; Mismatches 13; Indels 17; Gaps 1;

Qy 1 MAPSGLRLLPLLPLWLLVLTGPRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKRLA 60

Db 1 MPPSGRLRLPLLLPLLWLLMLTPGRPVAGLSTCKTIDMELVKRKGIEAIRGOILSKLRLA 60

Qy 61 SPPSQGDVPPGGLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNOI 120

Db 61 SPPSQGDVPPGGLPEAILALYNSTRDRVAGESAETEPEPEADYYAKEVTRVLMVEYGNKI 120

Qy 121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLRLKLVKVEQHVELYQKYSNDSWR 180

Db 121 YDKMKSSSHSIYMFNTSELREAVPEPVLLSRADVRLRLKLKVEOHVELYQKYSNNSWR 180

Qy 181 YLSNRLLAPSDSPEWLSFDVTGVVROWLTRREAI EGFRLSAHCSCDSKDN TLHVEINGFN 240

```

      |||
Db      181 YLSNRL LAPSDSPEWLSFDVTGVVROWLTHREEIEGFRLSAHCSDSKDNTLOVDINGFS 240

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Qv 241 SGRRGDLATIHGMNRPFLLLMATPLERAOHLHSSRHRRAALDTNSYPYDVPDYASLALDTN 300

Db	241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRR-----ALDTN	283
Qy	301 YCFSSTEKNCCVRQLYIDFRKDLGWKIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY	360
Db	284 YCFSSTEKNCCVRQLYIDFRKDLGWKIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY	343
Qy	361 NQHNP GASAAPCCVPQALEPLPIVYYVG RKP KVEQLSNMIVRSCKCS	407
Db	344 NQHNP GASAAPCCVPQALEPLPIVYYVG RKP KVEQLSNMIVRSCKCS	390

Query Match 89.7%; Score 1946.5; DB 15; Length 390;
Best Local Similarity 90.4%; Pred. No. 3.7e-173;
Matches 368; Conservative 10; Mismatches 12; Indels 17; Gaps 1;

RESULT 6

US-09-214-592-33

; Sequence 33, Application US/09214592A
; Publication No. US20030027218A1
; GENERAL INFORMATION:
; APPLICANT: Yamasaki,CMotoo
; APPLICANT: Shibata,CKenji
; APPLICANT: Sato,CYasufumi
; TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND
METHOD
; TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS
; FILE REFERENCE: 11060
; CURRENT APPLICATION NUMBER: US/09/214,592A
; CURRENT FILING DATE: 1999-01-18
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE:
; SEQ ID NO 33
; LENGTH: 390
; TYPE: PRT
; ORGANISM: simian
US-09-214-592-33

Query Match 89.2%; Score 1934.5; DB 11; Length 390;
Best Local Similarity 89.9%; Pred. No. 4.9e-172;
Matches 366; Conservative 10; Mismatches 14; Indels 17; Gaps 1;

Qy	1	MAPSGRLRLPLLLPLLWLLVLTGPRPAAGLSTCKTIDMELVKKRIEAI	RGQILSKLRLA	60
Db	1	MPPSGRLRLPLLLPLLWLLVLTGPRPAAGLSTCKTIDMELVKKRIEAI	RGQILSKLRLA	60
Qy	61	SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEV	TRVLMVESGNQI	120
		:		
Db	61	SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEV	TRVLMVETHNEI	120
		:		
Qy	121	YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQH	VELYQKYSNDSWR	180
		: :		
Db	121	YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKLKVEQH	VELYQKYSNNSWR	180
		: :		
Qy	181	YLSNRL LAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHCSCDS	SKDNTLHVEINGFN	240
		:		
Db	181	YLSNRL LAPSNSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDS	SKDNTLQVDINGFT	240
		:		
Qy	241	SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNSYPY	DVPDYASLALDTN	300
		:		
Db	241	TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR-----	ALDTN	283
Qy	301	YCFSSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYI	WSLDTQYSKVLALY	360
Db	284	YCFSSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYI	WSLDTQYSKVLALY	343
Qy	361	NQHNP GASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS		407
Db	344	NQHNP GASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS		390

RESULT 7


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; Patent No. US20020151478A1
; GENERAL INFORMATION:
; APPLICANT: Chernajovsky, Yuti
; APPLICANT: Dreja, Hanna Stina
; APPLICANT: Adams, Gillian
; TITLE OF INVENTION: Latent Fusion Protein
; FILE REFERENCE: 0623.1000000
; CURRENT APPLICATION NUMBER: US/09/756,283A
; CURRENT FILING DATE: 2001-01-09
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-756-283A-23
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Query Match          88.8%; Score 1925.5; DB 10; Length 390;
Best Local Similarity 89.7%; Pred. No. 3.4e-171;
Matches 365; Conservative 10; Mismatches 15; Indels 17; Gaps 1;
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Qy      1 MAPSGLRLLPLLLPLWLLVLTGPRPAAGLSTCKTIDMELVKRKRIEAIHQILSKLRLA 60
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1 MPPSGLRLLPLLLPLWLLVLTGPFPAAAGLSTCKTIDMELVKRKRIEAIHQILSKLRLA 60

Qy     61 SPSPQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
      | | | | | : | | | | | | | | | | | | | | | | | | | | | : : |
Db     61 SPSPQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHHEI 120

Qy    121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLVKVEQHVELYQKYSNDSWR 180
      | | | | : | | | | | | | | | | | | | | | | | | | | | : | |
Db    121 YDKFKQSTHSTYMFNISELREAVPEPVLLSRAELRLLRLKLVKVEQHVELYQKYSNNSWR 180

Qy    181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHCSCDSKDNTLHVEINGFN 240
      | | | | | | | | | | | | | | | : | | | | | | | | | : | | | |
Db    181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFT 240

Qy    241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNSYPYDVPDYASLALDTN 300
      : | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR-----ALDTN 283

Qy    301 YCFSSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 360
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    284 YCFSSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 343

Qy    361 NQHNPASAAAPCCVPQALEPLPIVYVGRKPKVEQLSNMIVRSCKCS 407
      | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    344 NQHNPASAAAPCCVPQALEPLPIVYVGRKPKVEQLSNMIVRSCKCS 390
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RESULT 9
US-09-214-592-28
; Sequence 28, Application US/09214592A
; Publication No. US20030027218A1
; GENERAL INFORMATION:
; APPLICANT: Yamasaki, CMotoo
; APPLICANT: Shibata, CKenji
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```

; APPLICANT: Sato,CYasufumi
; TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND
METHOD
; TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS
; FILE REFERENCE: 11060
; CURRENT APPLICATION NUMBER: US/09/214,592A
; CURRENT FILING DATE: 1999-01-18
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE:
; SEQ ID NO 28
; LENGTH: 390
; TYPE: PRT
; ORGANISM: canine
US-09-214-592-28

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Qy	1	MPSGLRLLPLLLPLLWLVLTGPRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKRLA	60
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Db	1	MPPSGLRLLPLLLPLLWLVLTGPRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKRLS	60
Qy	61	SPPSQGDVPPGPPLPEAVIALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVL MVESGNQI	120
		: : :	
Db	61	SPPSQGEVPPVPPLPEAVIALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVL MVENTNKI	120
Qy	121	YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLVKEQHVELYQKYSNDSWR	180
		: : :	
Db	121	YEKVKKSPHSIYMLFNTSELREAVPEPVLLSRAELRLLRLKLKAEQHVELYQKYSNDSWR	180
Qy	181	YLSNRLLAPSDSPEWL SFDVTGVVRQWL TRREA IEGFRLSAHCS CDSKDNTLHVEINGFN	240
		: : : :	
Db	181	YLSNRLLAPSDTPEWL SFDVTGVVRQWL SHGGEVEGFRLSAHCSCDSKDNTLQVDINGFS	240
Qy	241	SGRRGDLATI HGMNRP FLLL MATPLERA QHLHSS RHRRALD TNSYPDV PDYAS LALDTN	300
Db	241	SSRRGDLATI HGMNRP FLLL MATPLERA QHLHSS RQR-----ALDTN	283
Qy	301	YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY	360
Db	284	YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY	343
Qy	361	NQHNP GASAAPCCVPQALEPLPI VVVGRKP KVEQLSNMI VRSC KCS	407
Db	344	NOHNPGAS AAPCCVPQALEPLPI VVVGRKP KVEQLSNMI VRSC KCS	390

```

; TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND
METHOD
; TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS
; FILE REFERENCE: 11060
; CURRENT APPLICATION NUMBER: US/09/214,592A
; CURRENT FILING DATE: 1999-01-18
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE:
; SEQ ID NO 20
; LENGTH: 390
; TYPE: PRT
; ORGANISM: murine
US-09-214-592-20

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Query Match          85.5%; Score 1855.5; DB 11; Length 390;
Best Local Similarity 85.5%; Pred. No. 1.2e-164;
Matches 348; Conservative 15; Mismatches 27; Indels 17; Gaps 1;

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Qy      1 MAPSGLRLLPLLLPLWLLVLTTPGRPAAGLSTCKTIDMELVKRKRIEAIHQILSKLRLA 60
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1 MPPSGLRLLPLLLPLWLLVLTTPGRPAAGLSTCKTIDMELVKRKRIEAIHQILSKLRLA 60

Qy     61 SPSPQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
      | | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     61 SPSPQGEVPPGPLPEAVLALYNSTRDRVAGESADPEPEPEADYYAKEVTRVLMVDRNNAI 120

Qy    121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
      | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    121 YEKTKDISHSIYMFNTSDIREAVPEPPLLSRAELRLQLRKSSVEQHVELYQKYSNNSWR 180

Qy    181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHCSCDSKDNLTlhVEINGFN 240
      | | | | | | : | : | | | | | | | | | | | | | | | | | | | | :
Db    181 YLGNRLLTPDTPDWLSFDVTGVVRQWLNQGDGIQGRFRSAHCSCDSKDNKLHVEINGIS 240

Qy    241 SGRRGDLATIHGMRNPFLLLMATPLERAQHLHSSRRHRRALDTNSYPYDVPDYASLALDTN 300
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    241 PKRRGDLGTIHDNRNPFLLLMATPLERAQHLHSSRRHRR-----ALDTN 283

Qy    301 YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 360
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    284 YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 343

Qy    361 NQHNPASAAAPCCVPQALEPLPIVYVGRKPKVEQLSNMIVRSCKCS 407
      | | | | | | | : | | | | | | | | | | | | | | | | | | | |
Db    344 NQHNPASASPCCVPQALEPLPIVYVGRKPKVEQLSNMIVRSCKCS 390

```

RESULT 11

```

US-09-214-592-23
; Sequence 23, Application US/09214592A
; Publication No. US20030027218A1
; GENERAL INFORMATION:
; APPLICANT: Yamasaki,CMotoo
; APPLICANT: Shibata,Ckenji
; APPLICANT: Sato,Cyasufumi
; TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND
METHOD

```



```
; TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS
; FILE REFERENCE: 11060
; CURRENT APPLICATION NUMBER: US/09/214,592A
; CURRENT FILING DATE: 1999-01-18
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE:
; SEQ ID NO 23
; LENGTH: 390
; TYPE: PRT
; ORGANISM: rat
US-09-214-592-23
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Query Match          85.5%;  Score 1855.5;  DB 11;  Length 390;
Best Local Similarity 85.5%;  Pred. No. 1.2e-164;
Matches 348;  Conservative 14;  Mismatches 28;  Indels 17;  Gaps 1;
```

```
QY      1 MAPSGLRLLPLLLPLLWLLVLTTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKRLA 60
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1 MPPSGLRLLPLLLPLPWLLVLTTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKRLA 60

QY     61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
      | | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESADPEPEPEPEADYYAKEVTRVLMVDRNNAI 120

QY    121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLVKVEQHVELYQKYSNDSWR 180
      | | | | | : | | : | | | | | : | | | | | | | | | | | | | | | | |
Db    121 YDKTKDITHSIYMFNTSDIREAVPEPPLLSRAELRLQRFKSTVEQHVELYQKYSNNNSWR 180

QY    181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHCSCDSKDNTLHVEINGFN 240
      | | | | | : | | : | | | | | | | | | | | | | | | | | | | | | |
Db    181 YLGNRLLTPTDTPWLSFDVTGVVRQWLNQGDGIQGFRFSAHCSCDSKDNVLHVEINGIS 240

QY    241 SGRRGDLATIHGMRNPFLLLMATPLERAQHLHSSRHRRALDTNSYPYDVPDYASLALDTN 300
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    241 PKRRGDLGTIHDNRPFLLLMATPLERAQHLHSSRHRR-----ALDTN 283

QY    301 YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 360
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    284 YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 343

QY    361 NQHNPASAAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    344 NQHNPASASPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
```

RESULT 12

US-09-214-592-25

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; Sequence 25, Application US/09214592A
; Publication No. US20030027218A1
; GENERAL INFORMATION:
; APPLICANT: Yamasaki,CMotoo
; APPLICANT: Shibata,CKenji
; APPLICANT: Sato,CYasufumi
; TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND
METHOD
; TITLE OF INVENTION: OF SCREENING TGF- ACTIVITY-REGULATING COMPOUNDS
; FILE REFERENCE: 11060
```

; CURRENT APPLICATION NUMBER: US/09/214,592A
; CURRENT FILING DATE: 1999-01-18
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE:
; SEQ ID NO 25
; LENGTH: 315
; TYPE: PRT
; ORGANISM: bovine
US-09-214-592-25

Query Match 73.4%; Score 1592.5; DB 11; Length 315;
Best Local Similarity 89.5%; Pred. No. 3.1e-140;
Matches 297; Conservative 9; Mismatches 9; Indels 17; Gaps 1;

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Qy      76  AVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQIYDKFKGTPHSLYMLF 135
      |:|||||
Db      1  AILALYNSTRDRVAGESAETEPEPEADYYAKEVTRVLMVEYGNKIYDKMKSSSHSIYMFF 60

Qy     136  NTSELREAVPEPVLLSRAELRLLRLKLVQEHVELYQKYSNDSWRYLNSRLLAPSDSPEW 195
      |||||
Db      61  NTSELREAVPEPVLLSRADVRLRLKLVQEHVELYQKYSNNSWRYLNSRLLAPSDSPEW 120

Qy     196  LSFDTVGVVRQWLTRREAIEGFRLSAHCSCDSKDNTHLVEINGFNSGRRGDLATIHGMNR 255
      |||||
Db     121  LSFDTVGVVRQWLTRREEIEGFRLSAHCSCDSKDNTHLQVDINGFSSGRRGDLATIHGMNR 180

Qy     256  PFLLLMATPLERAQHLHSSRHRRALDTNSYPYDVPDYASLALDTNYCFSSTEKNCCVRQL 315
      |||||
Db     181  PFLLLMATPLERAQHLHSSRHR-----ALDTNYCFSSTEKNCCVRQL 223

Qy     316  YIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPASAAAPCCVP 375
      |||||
Db     224  YIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPASAAAPCCVP 283

Qy     376  QALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
      |||||
Db     284  QALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 315
```

RESULT 13
US-09-756-283A-20
; Sequence 20, Application US/09756283A
; Patent No. US20020151478A1
; GENERAL INFORMATION:
; APPLICANT: Chernajovsky, Yuti
; APPLICANT: Dreja, Hanna Stina
; APPLICANT: Adams, Gillian
; TITLE OF INVENTION: Latent Fusion Protein
; FILE REFERENCE: 0623.1000000
; CURRENT APPLICATION NUMBER: US/09/756,283A
; CURRENT FILING DATE: 2001-01-09
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Artificial Sequence

Db	190	PLGLW----AGGGSAALSTCKTIDMELVKKRIEAIRGQILSKRLASPPSQGEVPPGP	245
Qy	73	LPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMEVSGNQIYDKFKGTPHSLY	132
		: : : :	
Db	246	LPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEIYDKFKQSTHSIY	305
Qy	133	MLFNTSELREAVPEPVLLSRAELRLL-RLKLKVEQHVELYQKYSNDSWRYLSNRLLAPSD	191
		:	
Db	306	MFFNTSELREAVPEPVLLSRAELRLLRRLKLKVEQHVELYQKYSNNSWRYLSNRLLAPSD	365
Qy	192	SPEWL SFDVTGVVRQWLTRREAIEGFRLSAHCSCDSKDNTLHVEINGFN SGRRGDLATIH	251
		: : :	
Db	366	SPEWL SFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFTTGRRGDLATIH	425
Qy	252	GMNRPFLLLMATPLERAQHLHS	273
Db	426	GMNRPFLLLMATPLERAOHLOS	447

US-09-214-592-32

; Sequence 32, Application US/09214592A

; GENERAL INFORMATION:

; APPLICANT: Shibata, CKenji

; TITLE OF INVENTION: PEPTIDES WHICH PROMOTE ACTIVATION OF LATENT TGF- AND
METHOD

FILE REFERENCE: 11060

; CURRENT FILING DATE: 1999-01-18

; SOFTWARE:

; LENGTH: 373

; ORGANISM: chicken

Query Match 49.2%; Score 1067; DB 11; Length 373;

Matches 209; Conservative 52; Mismatches 98; Indels 32; Gaps 8;

```

Qy      204 VRQWLTRREAIEGFRLSAHCSCD---SKDNTLHVEINGFNSGRRGDLATIHGMNR--PFL 258
      | |||: | : || || |:      : : || | :|||: :| :| |::
Db      181 VHQLSGSELLGVFKLSVHCPCEMGPGHAEEMRISIEGFEQ-QRGDMQSIKKHRRVPYV 239

Qy      259 LLMATPLERAQHLHSSRRRRALDTNSYPYDVPDYASIALDTNYCF--SSTEKNCCVRQLY 316
      | || | ||| |||:| ||      |||:||| : ||||| |||
Db      240 LAMALPAERANELHSARRRR-----DLDTDYCFGPGTDEKNCCVRPLY 282

Qy      317 IDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPASAAAPCCVPQ 376
      ||||| ||||| |||||:||||| |||||:||||| ||||| |||||
Db      283 IDFRKDLQWKWIHEPKGYMANFCMGPCPYIWSADTQYTKVLALYNQHNPASAAAPCCVPQ 342

Qy      377 ALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
      |:|||:||||| :|||||:|:|:|
Db      343 TLDPLPIIYYVGRNVRVEQLSNMIVRACKCS 373

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Search completed: October 28, 2003, 09:28:02
Job time : 24.6934 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 28, 2003, 00:37:16 ; Search time 13.4491 Seconds
(without alignments)
2910.285 Million cell updates/sec

Title: US-10-017-372E-39
Perfect score: 2169
Sequence: 1 MAPSGLRLLPLLLPLWLLV.....GRKPKVEQLSNMIVRSCKCS 407

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	2053.5	94.7	390	2	A27512	transforming growth	
2	2022	93.2	391	2	S01413	transforming growth	
3	1949.5	89.9	390	2	I46463	transforming growth	
4	1936.5	89.3	390	1	WFHU2	transforming growth	
5	1934.5	89.2	390	2	A26960	transforming growth	
6	1913.5	88.2	390	2	JC4023	transforming growth	
7	1855.5	85.5	390	1	WFMS2	transforming growth	
8	1855.5	85.5	390	2	S10219	transforming growth	
9	1592.5	73.4	315	2	A40057	transforming growth	
10	1067	49.2	373	2	A41918	transforming growth	
11	888.5	41.0	412	2	A34939	transforming growth	
12	887.5	40.9	382	2	B61036	transforming growth	
13	851	39.2	409	2	S01825	transforming growth	
14	844.5	38.9	410	2	A41397	transforming growth	
15	844	38.9	414	1	WFMSE2	transforming growth	
16	843.5	38.9	410	2	A55706	transforming growth	
17	841.5	38.8	412	2	A36169	transforming growth	
18	829	38.2	414	1	WFMKB2	transforming growth	
19	829	38.2	414	2	A31249	transforming growth	
20	828.5	38.2	413	1	WFXLB2	transforming growth	
21	825	38.0	412	2	A39489	transforming growth	
22	813	37.5	442	2	B31249	transforming growth	
23	691.5	31.9	130	2	I48196	transforming growth	
24	482	22.2	112	2	A61439	transforming growth	
25	275	12.7	425	2	I47072	inhibin beta-A chain	
26	270.5	12.5	424	1	WFPGBA	inhibin beta-A chain	
27	270	12.4	425	1	S50898	inhibin beta-A chain	
28	268.5	12.4	424	1	S31440	inhibin beta-A chain	
29	264.5	12.2	424	1	B40905	inhibin beta-A chain	
30	262.5	12.1	426	1	B24248	inhibin beta-A chain	
31	256.5	11.8	513	1	BMHU6	bone morphogenetic	
32	253.5	11.7	413	2	JC4862	activin beta-A chain	
33	251.5	11.6	398	2	JH0688	bone morphogenetic	
34	250	11.5	394	2	S45355	bone morphogenetic	
35	250	11.5	398	2	JH0687	bone morphogenetic	
36	249	11.5	396	1	BMHU2	bone morphogenetic	
37	246	11.3	510	2	A54798	Vg-1-related protein	
38	244	11.2	455	2	A43918	TGF-beta-related protein	
39	241.5	11.1	393	2	S37073	bone morphogenetic	
40	238	11.0	350	2	JC5241	activin beta E chain	
41	236	10.9	407	1	A40150	inhibin beta-B chain	
42	234.5	10.8	402	2	A45056	osteogenic protein	
43	232	10.7	411	2	B41398	inhibin beta-B chain	
44	229	10.6	393	2	I50103	activin beta B - z	
45	229	10.6	420	2	I49541	bone morphogenetic	

ALIGNMENTS

A27512
transforming growth factor beta-1 precursor - pig
N;Alternate names: TGF-beta
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 16-Jul-1999
C;Accession: A27512; A26356; I46657
R;Derynck, R.; Rhee, L.
Nucleic Acids Res. 15, 3187, 1987
A;Title: Sequence of the porcine transforming growth factor-beta precursor.
A;Reference number: A27512; MUID:87174844; PMID:3470708
A;Accession: A27512
A;Molecule type: mRNA
A;Residues: 1-390 <DER>
R;Cheifetz, S.; Weatherbee, J.A.; Tsang, M.L.S.; Anderson, J.K.; Mole, J.E.;
Lucas, R.; Massague, J.
Cell 48, 409-415, 1987
A;Title: The transforming growth factor-beta system, a complex pattern of cross-
reactive ligands and receptors.
A;Reference number: A90890; MUID:87102890; PMID:2879635
A;Accession: A26356
A;Molecule type: protein
A;Residues: 279-322 <CHE>
R;Kondaiah, P.; Van Obberghen-Schilling, E.; Ludwig, R.L.; Dhar, R.; Sporn,
M.B.; Roberts, A.B.
J. Biol. Chem. 263, 18313-18317, 1988
A;Title: cDNA cloning of porcine transforming growth factor-beta 1 mRNAs.
Evidence for alternate splicing and polyadenylation.
A;Reference number: I46657; MUID:89054010; PMID:2461367
A;Accession: I46657
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-390 <KON>
A;Cross-references: GB:M23703; NID:g755044; PIDN:AAA64616.1; PID:g755045
C;Genetics:
A;Gene: TGFB; TGF-beta-1
C;Superfamily: inhibin
C;Keywords: growth factor

Query Match 94.7%; Score 2053.5; DB 2; Length 390;
Best Local Similarity 95.6%; Pred. No. 2.1e-158;
Matches 389; Conservative 0; Mismatches 1; Indels 17; Gaps 1;

Qy	1	MAPSGLRLLPLLLPLLWLLVLT	TPGRPAAGLSTCKTIDMELVKRKRIE	AIRGQILSKLRLA	60
Db	1	MPPSGLRLLPLLLPLLWLLVLT	TPGRPAAGLSTCKTIDMELVKRKRIE	AIRGQILSKLRLA	60
Qy	61	SPPSQGDVPPGPLPEAVLALYNSTR	DRVAGESVEPEPEPEADYYAKEVTR	VLMMVESGNQI	120
Db	61	SPPSQGDVPPGPLPEAVLALYNSTR	DRVAGESVEPEPEPEADYYAKEVTR	VLMMVESGNQI	120
Qy	121	YDKFKGTPHSLYMLFNTSELREAVPEP	VLLSRAELRLLRLKLKVEQHVELYQKYSN	DSWR	180
Db	121	YDKFKGTPHSLYMLFNTSELREAVPEP	VLLSRAELRLLRLKLKVEQHVELYQKYSN	DSWR	180
Qy	181	YLSNRL LAPSDSPEWLSFDVTGVVRQWL	TRREAIEGFRLSAHCSCDSKDNTLHVEINGFN	240	
Db	181	YLSNRL LAPSDSPEWLSFDVTGVVRQWL	TRREAIEGFRLSAHCSCDSKDNTLHVEINGFN	240	

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Qy      241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNSYPYDVPDYASIALDTN 300
      |||
Db      241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRR-----ALDTN 283

Qy      301 YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 360
      |||
Db      284 YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 343

Qy      361 NQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
      |||
Db      344 NQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390

```

RESULT 2

S01413

transforming growth factor beta-1 precursor - chicken

C;Species: Gallus gallus (chicken)

C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 24-Nov-1999

C;Accession: S01413

R;Jakowlew, S.B.; Dillard, P.J.; Sporn, M.B.; Roberts, A.B.

Nucleic Acids Res. 16, 8730, 1988

A;Title: Nucleotide sequence of chicken transforming growth factor-beta 1 (TGF-beta 1).

A;Reference number: S01413; MUID:88335639; PMID:3166520

A;Accession: S01413

A;Molecule type: DNA

A;Residues: 1-391 <JAK>

A;Cross-references: EMBL:X12373; NID:g63808; PIDN:CAA30933.1; PID:g63809

C;Superfamily: inhibin

C;Keywords: growth factor

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Query Match          93.2%;  Score 2022;  DB 2;  Length 391;
Best Local Similarity 94.6%;  Pred. No. 7.6e-156;
Matches 386;  Conservative 0;  Mismatches 4;  Indels 18;  Gaps 2;

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Qy      1 MAPSGLRLLPLLLPLLWLLVLTTPGRPAAGLSTCKTIDMELVKKRIEAIRGQILSKLRLA 60
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Db      1 MPPSGPGLLPLLLPLLWLLVLTTPGRPAAGLSTCKTIDMELVKKRIEAIRGQILSKLRLA 60

Qy      61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
      |||
Db      61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120

Qy      121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
      |||
Db      121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWG 180

Qy      181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHCSCDSKDNTLHVEIN-GF 239
      |||
Db      181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHCSCDSKDNTLHVEINAGF 240

Qy      240 NSGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNSYPYDVPDYASLALDT 299
      |||
Db      241 NSGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRR-----ALDT 283

Qy      300 NYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLAL 359

```


Db 284 NYCFSSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLAL 343
 Qy 360 YNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
 Db 344 YNOHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 391

RESULT 3

I46463

transforming growth factor beta-1 - sheep

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 19-Dec-1997 #sequence revision 19-Dec-1997 #text change 24-Nov-1999

C;Accession: I46463; S45115

R; Woodall, C.J.; McLaren, L.J.; Watt, N.J.

Gene 150, 371-373, 1994

A;Title: Sequence and chromosomal localisation of the gene encoding ovine latent transforming growth factor-beta 1.

A;Reference number: I46463; MUID:95121932; PMID:7821809

A;Accession: I46463

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-390 <WOO>

A;Cross-references: EMBL:X76916; NID:q496648; PIDN:CAA54242.1; PID:q496649

A;Note: submitted to the EMBL Data Library, December 1993

C;Superfamily: inhibin

Query Match 89.9%; Score 1949.5; DB 2; Length 390;
Best Local Similarity 90.2%; Pred. No. 5.6e-150;
Matches 367; Conservative 10; Mismatches 13; Indels 17; Gaps 1;

[illegible]

Db

344 NQHNP GASAAPCCVPQALEPLIVYYVGRKPKVEQLSNMIVRSCKCS 390

RESULT 4

WFHU2

transforming growth factor beta-1 precursor [validated] - human

N;Alternate names: growth-inhibitory factor; TGF type 2; TGF-beta

C;Species: Homo sapiens (man)

C;Date: 28-Feb-1986 #sequence_revision 19-Oct-1995 #text_change 08-Dec-2000

C;Accession: A27513; A01395; A22290; I59664; S53444

R;Derynck, R.; Rhee, L.; Chen, E.Y.; Van Tilburg, A.

Nucleic Acids Res. 15, 3188-3189, 1987

A;Title: Intron-exon structure of the human transforming growth factor-beta precursor gene.

A;Reference number: A27513; MUID:87174845; PMID:3470709

A;Accession: A27513

A;Molecule type: DNA

A;Residues: 1-390 <DER>

A;Cross-references: GB:X05839; GB:Y00112; NID:g37097; PIDN:CAA29283.1;

PID:g1212989

R;Derynck, R.; Jarrett, J.A.; Chen, E.Y.; Eaton, D.H.; Bell, J.R.; Assoian, R.K.; Roberts, A.B.; Sporn, M.B.; Goeddel, D.V.

Nature 316, 701-705, 1985

A;Title: Human transforming growth factor-beta complementary DNA sequence and expression in normal and transformed cells.

A;Reference number: A01395; MUID:85296301; PMID:3861940

A;Accession: A01395

A;Molecule type: mRNA

A;Residues: 1-9,'P',11-24,'P',26-159,'R',160-390 <DE2>

A;Cross-references: GB:X02812; GB:J05114; NID:g37092; PIDN:CAA26580.1;

PID:g37093

A;Note: the authors suggest that residues 8-23 could represent the hydrophobic core of an amino-terminal signal peptide

R;Massague, J.; Like, B.

J. Biol. Chem. 260, 2636-2645, 1985

A;Title: Cellular receptors for type beta transforming growth factor. Ligand binding and affinity labeling in human and rodent cell lines.

A;Reference number: A22290; MUID:85131019; PMID:2982829

A;Accession: A22290

A;Molecule type: protein

A;Residues: 279-295,'XX',298-301 <MAS>

R;Urushizaki, Y.; Niitsu, Y.; Terui, T.; Koshida, Y.; Mahara, K.; Kohgo, Y.; Urushizaki, I.; Takahashi, Y.; Ito, H.

Tumor Res. 22, 41-55, 1987

A;Title: Cloning and expression of the gene for human transforming growth factor-beta in Escherichia coli.

A;Reference number: I59664

A;Accession: I59664

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 279-390 <RES>

A;Cross-references: GB:M38449; NID:g339557; PIDN:AAA36735.1; PID:g339558

R;Stam, K.; Stewart, A.A.; Qu, G.Y.; Iwata, K.K.; Fenyoe, D.; Chait, B.T.; Marshak, D.R.; Haley, J.D.

Biochem. J. 305, 87-92, 1995

A;Title: Physical and biological characterization of a growth-inhibitory activity purified from the neuroepithelioma cell line A673.

A;Reference number: S53444; MUID:95126934; PMID:7826358
 A;Accession: S53444
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 279-297 <STA>
 C;Comment: The mature protein is the carboxyl-terminal segment of a precursor polypeptide; the active molecule is a dimer of identical polypeptide chains linked by an interchain disulfide bond.
 C;Genetics:
 A;Gene: GDB:TGFB1; TGFB
 A;Cross-references: GDB:120729; OMIM:190180
 A;Map position: 19q13.2-19q13.2
 C;Superfamily: inhibin
 C;Keywords: glycoprotein; growth factor; homodimer; mitogen; transformation
 F;1-18/Domain: signal sequence #status predicted <SIG>
 F;19-278/Domain: propeptide #status predicted <PRO>
 F;244-246/Region: cell attachment (R-G-D) motif
 F;279-390/Product: transforming growth factor beta-1 #status experimental <MAT>
 F;82,136,176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 89.3%; Score 1936.5; DB 1; Length 390;
 Best Local Similarity 90.2%; Pred. No. 6.3e-149;
 Matches 367; Conservative 10; Mismatches 13; Indels 17; Gaps 1;

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Qy      1 MAPSGLRLLPLLLPLLWLLVLTGPRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1 MPPSGLRLLLLLLPLLWLLVLTGPRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60

Qy     61 SPSPQGDVPPGGLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
      | | | | | : | | | | | | | | | | | | | | | | | | | | | | | |
Db     61 SPSPQGEVPPGGLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120

Qy    121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
      | | | | : | | : | | | | | | | | | | | | | | | | | | | | |
Db    121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNNSWR 180

Qy    181 YLSNRLLAPSDSPEWLSFDVTVGVVRQWLTRREAI EGFRLSAHCSCDSKDNTLHVEINGFN 240
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    181 YLSNRLLAPSDSPEWLSFDVTVGVVRQWLSRGGEI EGFRLSAHCSCDSRDNTLQVDINGFT 240

Qy    241 SGRRGDLATIHGMNRPFLLL MATPLERAQHLHSSRHRRALDTNSYPYDVPDYASLALDTN 300
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    241 TGRRGDLATIHGMNRPFLLL MATPLERAQHLQSSRHRR-----ALDTN 283

Qy    301 YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 360
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    284 YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 343

Qy    361 NQHNP GASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    344 NQHNP GASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
  
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RESULT 5
 A26960
 transforming growth factor beta-1 precursor - green monkey
 C;Species: Cercopithecus aethiops (green monkey, grivet)

C;Date: 05-Oct-1988 #sequence_revision 05-Oct-1988 #text_change 24-Nov-1999
 C;Accession: A26960
 R;Sharples, K.; Plowman, G.D.; Rose, T.M.; Twardzik, D.R.; Purchio, A.F.
 DNA 6, 239-244, 1987
 A;Title: Cloning and sequence analysis of simian transforming growth factor-beta
 cDNA.
 A;Reference number: A26960; MUID:87246074; PMID:3474130
 A;Accession: A26960
 A;Molecule type: mRNA
 A;Residues: 1-390 <SHA>
 A;Cross-references: GB:M16658; NID:g176552; PIDN:AAA35369.1; PID:g176553
 C;Superfamily: inhibin
 C;Keywords: growth factor
 F;1-16/Domain: signal sequence #status predicted <SIG>
 F;17-390/Product: transforming growth factor beta #status predicted <MAT>

Query Match 89.2%; Score 1934.5; DB 2; Length 390;
 Best Local Similarity 89.9%; Pred. No. 9.1e-149;
 Matches 366; Conservative 10; Mismatches 14; Indels 17; Gaps 1;

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Qy      1 MAPSGLRLLPLLLPLLWLLVLTTPGRPAAGLSTCKTIDMELVKRKRIEAI RQILSKLRLA 60
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1 MPPSGLRLLPLLLPLLWLLVLTTPSRPAAGLSTCKTIDMELVKRKRIETIR QILSKLRLA 60

Qy     61 SPSPQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
      | | | | : | | | | | | | | | | | | | | | | | | | | | | | : | |
Db     61 SPSPQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI 120

Qy    121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLVKVEQHVELYQKYSNDSWR 180
      | | | | : | | : | | | | | | | | | | | | | | | | | | | : | |
Db    121 YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKLVKVEQHVELYQKYSNNSWR 180

Qy    181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHCSCDSKDNTLHVEINGFN 240
      | | | | | | | : | | | | | | | | | | : | | | | | | | | | | | : | |
Db    181 YLSNRLLAPSNSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSKDNTLQVDINGFT 240

Qy    241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNSYPYDVPDYASLALDTN 300
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    241 TGRRGDLATIHGMNRPFLLLMATPLERAQHLQSSRHRR-----ALDTN 283

Qy    301 YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 360
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    284 YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 343

Qy    361 NQHNPASAAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    344 NQHNPASAAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390

```

RESULT 6
 JC4023
 transforming growth factor beta-1 - dog
 C;Species: Canis lupus familiaris (dog)
 C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 24-Nov-1999
 C;Accession: JC4023
 R;Manning, A.M.; Auchampach, J.A.; Drong, R.F.; Slightom, J.L.
 Gene 155, 307-308, 1995

A;Title: The murine transforming growth factor-beta precursor.
A;Reference number: A01396; MUID:86168129; PMID:3007454
A;Accession: A01396
A;Molecule type: mRNA
A;Residues: 1-390 <DER>
A;Cross-references: GB:M13177; NID:g201952; PIDN:AAA40423.1; PID:g201953
A;Note: the authors suggest that residues 8-23 could represent the hydrophobic core of an amino-terminal signal peptide
C;Comment: The mature protein is the carboxyl-terminal segment of a precursor polypeptide; the active molecule is a dimer of identical polypeptide chains linked by an interchain disulfide bond.
C;Superfamily: inhibin
C;Keywords: glycoprotein; growth factor; growth regulation; homodimer; mitogen; transformation
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-278/Domain: propeptide #status predicted <PRO>
F;244-246/Region: cell attachment (R-G-D) motif
F;279-390/Product: transforming growth factor beta-1 #status predicted <MAT>
F;82,136,176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 85.5%; Score 1855.5; DB 1; Length 390;
Best Local Similarity 85.5%; Pred. No. 2.3e-142;
Matches 348; Conservative 15; Mismatches 27; Indels 17; Gaps 1;

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Qy      1 MAPSGLRLLPLLLPLWLLVLTGPRPAAGLSTCKTIDMELVKRKRIEAI RGQILSKLRLA 60
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1 MPPSGLRLLPLLLPLWLLVLTGPRPAAGLSTCKTIDMELVKRKRIEAI RGQILSKLRLA 60

Qy     61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
      | | | | | : | | | | | | | | | | | | | | | | | | | | | | | |
Db     61 SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESADPEPEPEPEADYYAKEVTRVLMVDRNNAI 120

Qy    121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLRLKLVKVEQHVELYQKYSNDSWR 180
      | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    121 YEKTKDISHSIYMFNTSDIREAVPEPPVLLSRAELRLQRLKSSVEQHVELYQKYSNNSWR 180

Qy    181 YLSNRLLAPSDSPEWLSFDVTVGVVQWLTRREAIEGFRLSAHCSCDSKDNTLHVEINGFN 240
      | | | | | | : | : | | | | | | | | | | | : : | : | | | | | | | :
Db    181 YLGNRLLTPTDTPWLSFDVTVGVVQWLNQGDGIQGFRFSAHCSCDSKDNKLHVEINGIS 240

Qy    241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNSYPYDVPDYASLALDTN 300
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    241 PKRRGDLGTIHDMNRPFLLLMATPLERAQHLHSSRHRR-----ALDTN 283

Qy    301 YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 360
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    284 YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 343

Qy    361 NQHNP GASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
      | | | | | | | : | | | | | | | | | | | | | | | | | | | | | |
Db    344 NQHNP GASASPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390

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RESULT 8
S10219
transforming growth factor beta-1 precursor - rat
N;Alternate names: TGF type 2; TGF-beta

C;Species: Rattus norvegicus (Norway rat)
 C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 24-Nov-1999
 C;Accession: S10219; PT0023; S02267
 R;Qian, S.W.; Kondaiah, P.; Roberts, A.B.; Sporn, M.B.
 Nucleic Acids Res. 18, 3059, 1990
 A;Title: cDNA cloning by PCR of rat transforming growth factor beta-1.
 A;Reference number: S10219; MUID:90272425; PMID:2349108
 A;Accession: S10219
 A;Molecule type: mRNA
 A;Residues: 1-390 <QIA>
 A;Cross-references: EMBL:X52498; NID:g57341; PIDN:CAA36741.1; PID:g57342
 R;Okada, F.; Yamaguchi, K.; Ichihara, A.; Nakamura, T.
 J. Biochem. 106, 304-310, 1989
 A;Title: Purification and structural analysis of a latent form of transforming growth factor-beta from rat platelets.
 A;Reference number: PT0023; MUID:90036779; PMID:2478527
 A;Accession: PT0023
 A;Molecule type: protein
 A;Residues: 30-32,'X',34-38,'Q',40-42,'X',44 <OKA>
 R;Okada, F.; Yamaguchi, K.; Ichihara, A.; Nakamura, T.
 FEBS Lett. 242, 240-244, 1989
 A;Title: One of two subunits of masking protein in latent TGF-beta is a part of pro-TGF-beta.
 A;Reference number: S02267; MUID:89121078; PMID:2914605
 A;Accession: S02267
 A;Molecule type: protein
 A;Residues: 30-32,'X',34-38,'Q',40-42,'X',44 <OK2>
 C;Superfamily: inhibin
 C;Keywords: glycoprotein; growth factor; integrin binding
 F;1-29/Domain: signal sequence #status predicted <SIG>
 F;30-278/Domain: propeptide #status experimental <PRO>
 F;244-246/Region: cell attachment (R-G-D) motif
 F;279-390/Product: transforming growth factor beta-1 #status predicted <MAT>
 F;82,136,176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 85.5%; Score 1855.5; DB 2; Length 390;
 Best Local Similarity 85.5%; Pred. No. 2.3e-142;
 Matches 348; Conservative 14; Mismatches 28; Indels 17; Gaps 1;

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Qy      1 MAPSGLRLLPLLLPLWLLVLTGPRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1 MPPSGLRLLPLLLPLPWLLVLTGPRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60

Qy     61 SPSPQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
      | | | | | : | | | | | | | | | | | | | | | | | | : | |
Db     61 SPSPQGEVPPGPLPEAVLALYNSTRDRVAGESADPEPEPEPEADYYAKEVTRVLMVDRNNAI 120

Qy    121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLRLKLVKVEQHVELYQKYSNDSWR 180
      | | | | | : | | | | | : | | | | | | | | | | | | : | |
Db    121 YDKTKDITHSIYMFNTSDIREAVPEPPLLSRAELRLQRFKSTVEQHVELYQKYSNNSWR 180

Qy    181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAI EGFRLSAHCSCDSKDNLTLHVEINGFN 240
      | | | | | : | | | | | | | | | | | | : : | | | | | | | | :
Db    181 YLGNRLLTPTDTPWLSFDVTGVVRQWLNQGDGIQGFRRSAHCSCDSKDNVLHVEINGIS 240

Qy    241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRRHRALDTNSYPYDVPDYASLALDTN 300
      | | | | | | | | | | | | | | | | | | | | | | | | | | |

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Db      241 PKRRGDLGTIHDNRPFLLLMATPLERAQHLHSSRHRR-----ALDTN 283
Qy      301 YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      284 YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 343
Qy      361 NQHNP GASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
        |||||:||||||||||||||||||||||||||
Db      344 NQHNP GASASPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390

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RESULT 9

A40057

transforming growth factor beta-1 precursor - bovine (fragment)

N;Alternate names: beta-TGF; cartilage-inducing factor-A; EGF-dependent TGF or dEGF; MGF-b; milk growth factor b; TGF-type II

C;Species: Bos primigenius taurus (cattle)

C;Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 16-Jul-1999

C;Accession: A40057; A42320; A05284; A24322; B61439

R;Van Obberghen-Schilling, E.; Kondaiah, P.; Ludwig, R.L.; Sporn, M.B.; Baker, C.C.

Mol. Endocrinol. 1, 693-698, 1987

A;Title: Complementary deoxyribonucleic acid cloning of bovine transforming growth factor-beta1.

A;Reference number: A40057; MUID:91042552; PMID:3153459

A;Accession: A40057

A;Molecule type: mRNA

A;Residues: 1-315 <VAN>

A;Cross-references: GB:M36271; NID:g163747; PIDN:AAA30778.1; PID:g163748

R;Ogawa, Y.; Schmidt, D.K.; Dasch, J.R.; Chang, R.J.; Glaser, C.B.

J. Biol. Chem. 267, 2325-2328, 1992

A;Title: Purification and characterization of transforming growth factor-beta2.3 and -beta1.2 heterodimers from bovine bone.

A;Reference number: A42320; MUID:92129307; PMID:1733936

A;Accession: A42320

A;Molecule type: protein

A;Residues: 204-209,'X',211-217 <OGA>

R;Roberts, A.B.; Anzano, M.A.; Meyers, C.A.; Wideman, J.; Blacher, R.; Pan, Y.C.E.; Stein, S.; Lehrman, S.R.; Smith, J.M.; Lamb, L.C.; Sporn, M.B.

Biochemistry 22, 5692-5698, 1983

A;Title: Purification and properties of a type beta transforming growth factor from bovine kidney.

A;Reference number: A05284; MUID:84104793; PMID:6607069

A;Accession: A05284

A;Molecule type: protein

A;Residues: 204-218 <ROB>

R;Seyedin, S.M.; Thompson, A.Y.; Bentz, H.; Rosen, D.M.; McPherson, J.M.; Conti, A.; Siegel, N.R.; Galluppi, G.R.; Piez, K.A.

J. Biol. Chem. 261, 5693-5695, 1986

A;Title: Cartilage-inducing factor-A. Apparent identity to transforming growth factor-beta.

A;Reference number: A24322; MUID:86195954; PMID:3754555

A;Accession: A24322

A;Molecule type: protein

A;Residues: 204-233 <SEY>

R;Jin, Y.; Cox, D.A.; Knecht, R.; Raschdorf, F.; Cerletti, N.

J. Protein Chem. 10, 565-575, 1991

A;Title: Separation, purification, and sequence identification of TGF-beta1 and TGF-beta2 from bovine milk.
A;Reference number: A61439; MUID:92189724; PMID:1799413
A;Accession: B61439
A;Molecule type: protein
A;Residues: 204-209,'X',211-217,'XX',220-232 <JIN>
C;Comment: This polypeptide is composed of two polypeptide chains cross-linked by disulfide bonds. It has been found in neoplastic and non-neoplastic tissues.
C;Comment: Type II TGF does not bind to the EGF receptor and lacks intrinsic mitogenic activity, but in soft agar, it reacts synergistically with either type I TFG or EGF, and induces cell proliferation. Cells grown in monolayer do not respond in a similar manner to these growth factors, but morphologically do acquire a transformed phenotype.
C;Superfamily: inhibin
C;Keywords: glycoprotein; growth factor; heterodimer
F;204-315/Product: transforming growth factor beta-1 #status experimental <MAT>
F;7,61,101/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 73.4%; Score 1592.5; DB 2; Length 315;
Best Local Similarity 89.5%; Pred. No. 3.2e-121;
Matches 297; Conservative 9; Mismatches 9; Indels 17; Gaps 1;

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Qy      76 AVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQIYDKFKGTPHSLYMLF 135
      |:||||||||||||||| | ||||||||||||||||| ||:|||| | : ||:|| |
Db      1 AILALYNSTRDRVAGESAETEPEPEADYYAKEVTRVLMVEYGNKIYDKMKSSSHSIYMF 60

Qy     136 NTSELREAVPEPVLLSRAELRLRLKLVKVEQHVELYQKYSNDSWRVLSNRL LAPSDSPEW 195
      |||||||||||||||:|||||||||||||:|||||||||
Db      61 NTSELREAVPEPVLLSRADVRLRLKLVKVEQHVELYQKYSNNSWRVLSNRL LAPSDSPEW 120

Qy     196 LSFDTVGVVRQWLTRREAIEGFRLSAHCSKCDKNTLHVEINGFNSGRRGDLATIHGMNR 255
      ||||||||||||||| | ||||||||||||||| |:||||:|||||
Db     121 LSFDTVGVVRQWLTRREEIEGFRLSAHCSKCDKNTLQVDINGFSSGRRGDLATIHGMNR 180

Qy     256 PFLLLMATPLERAQHLHSSRHRRALDTNSYPYDVPDYASLALDTNYCFSSTEKNCCVRQL 315
      ||||||||||||||| | |||||||||||||||
Db     181 PFLLLMATPLERAQHLHSSRHR-----ALDTNYCFSSTEKNCCVRQL 223

Qy     316 YIDFRKDLGKWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNP GASAAPCCVP 375
      ||||||||||||||| | |||||||||||||||
Db     224 YIDFRKDLGKWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNP GASAAPCCVP 283

Qy     376 QALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
      |||||||||||||||
Db     284 QALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 315

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RESULT 10

A41918
transforming growth factor beta-4 precursor - chicken (fragment)
N;Alternate names: TGF-beta 4
C;Species: Gallus gallus (chicken)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
C;Accession: A41918; A34941; S03110
R;Burt, D.W.; Jakowlew, S.B.
Mol. Endocrinol. 6, 989-992, 1992

QY 377 ALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
 |:||||:||||| :|||||||:|:|||||
 Db 343 TLDPLPIIYYVGRNVRVEQLSNMVVRACKCS 373

RESULT 11

A34939

transforming growth factor beta-3 precursor - chicken

C;Species: Gallus gallus (chicken)

C;Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 16-Jul-1999

C;Accession: A34939; S25850; S36125; S36124; I51181

R;Jakowlew, S.B.; Dillard, P.J.; Kondaiah, P.; Sporn, M.B.; Roberts, A.B.

Mol. Endocrinol. 2, 747-755, 1988

A;Title: Complementary deoxyribonucleic acid cloning of a novel transforming growth factor-beta messenger ribonucleic acid from chick embryo chondrocytes.

A;Reference number: A34939; MUID:89096966; PMID:3211158

A;Accession: A34939

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-412 <JAK>

A;Cross-references: GB:M31154; NID:g212758; PIDN:AAA49089.1; PID:g212759

R;Burt, D.W.; Paton, I.R.; Dey, B.R.

J. Mol. Endocrinol. 7, 175-183, 1991

A;Title: Comparative analysis of human and chicken transforming growth factor-beta-2 and -beta-3 promoters.

A;Reference number: S25850; MUID:92134496; PMID:1840616

A;Accession: S25850

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-117 <BUR>

A;Cross-references: EMBL:X58127; NID:g63815; PIDN:CAA41128.1; PID:g63816

A;Accession: S36125

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 119-172 <BU2>

A;Cross-references: EMBL:X60055; NID:g396688; PIDN:CAA42653.1; PID:g396689

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991

A;Accession: S36124

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 173-322,'ELPT',327-412 <BU3>

A;Cross-references: EMBL:X60091

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1991

R;Jakowlew, S.B.; Lechleider, R.; Geiser, A.G.; Kim, S.J.; Santa-Coloma, T.A.;

Cubert, J.; Sporn, M.B.; Roberts, A.B.

Mol. Endocrinol. 6, 1285-1298, 1992

A;Title: Identification and characterization of the chicken transforming growth factor-beta 3 promoter.

A;Reference number: I51181; MUID:93024487; PMID:1406706

A;Accession: I51181

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-117 <JA2>

A;Cross-references: GB:S46000; NID:g257172; PIDN:AAB23575.1; PID:g257173

C;Genetics:

A;Introns: 216/1; 252/1; 309/2; 360/3
A;Note: list of introns may be incomplete
C;Superfamily: inhibin
C;Keywords: glycoprotein; growth factor; growth regulation; homodimer; mitogen
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-300/Domain: propeptide #status predicted <PRO>
F;301-412/Product: transforming growth factor beta-3 #status predicted <MAT>
F;74,142/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 41.0%; Score 888.5; DB 2; Length 412;
Best Local Similarity 46.2%; Pred. No. 4.4e-64;
Matches 198; Conservative 56; Mismatches 114; Indels 61; Gaps 13;

```

Qy      15 LLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAI RQILSKLRLASPPSQGDVPPGGLP 74
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      9 LVLLSLLSFATVSLALSSCTTLDLEHIKKKRVEAI RQILSKLRLTSPPE--SVGPAHVP 66

Qy      75 EAVLALYNSTRDRVAGESVEPEPE-----PEADYYAKEVTRVLMVE---SGNQIYDKF 124
      : ||||| : : | : | | | : ||||| : : | : : | : :
Db      67 YQILALYNSTRELL--EEMEEKEEESCSQENTESEYYAKEIHKFDMIQGLPEHNELGICP 124

Qy     125 KGTPHSLYMLFNTSELREAVPEPVLLSRAELRLRL---KLKVEQHVELYQKYSND--- 177
      || : : | | | | | | | : ||| : || : | : | : | : |
Db     125 KGVTSNVFR-FNVS---SAEKNSTNLFRAEFRVLRVPNPSSKRSEQRIELFQILRPDEHI 180

Qy     178 -SWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHCSC-----D 226
      |||| | : ||||| ||| ||| ||| : | : | | | :
Db     181 AKQRYLSGRNVQTRGSPEWLSFDVTDTVREWLLHRESNLGLEISIHCPCHTFQPNGDILE 240

Qy     227 SKDNTLHVEINGFNSG---RRGDLATI---HGMNRPFLLLMATPLERAQH--LHSSRHRR 278
      : | : : | : | | | : : | : | | | : | : | : |
Db     241 NLHEVLEIKFKGIDSEDDYGRGDLGRLKKQKDLHNPHLILMMLPPHRLESPTLGGQRKKR 300

Qy     279 ALDTNSYPYDVPDYASIALDNTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANF 338
      ||||| : | : |||| | |||| : |||| : |||| | ||
Db     301 -----ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKQWVHEPKGYFANF 343

Qy     339 CLGPCPYIWSLDTQYSKVLALYNQHNP GASAAPCCVPQALEPLPIVYYVGRKPKVEQLSN 398
      | |||| : | | : | | | | | | ||| : |||| | |||| |
Db     344 CSGPCPYLRSADTTHSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSN 403

Qy     399 MIVRSCKCS 407
      | : | : ||||
Db     404 MVVKSCCKCS 412

```

RESULT 12

B61036

transforming growth factor beta-5 precursor - African clawed frog

C;Species: *Xenopus laevis* (African clawed frog)

C;Date: 31-Dec-1993 #sequence_revision 03-Feb-1994 #text_change 16-Jul-1999

C;Accession: A34929; B61036

R;Kondaiah, P.; Sands, M.J.; Smith, J.M.; Fields, A.; Roberts, A.B.; Sporn, M.B.; Melton, D.A.

J. Biol. Chem. 265, 1089-1093, 1990

A;Title: Identification of a novel transforming growth factor-beta (TGF-beta5) mRNA in *Xenopus laevis*.

A;Reference number: A34929; MUID:90110090; PMID:2295601
A;Accession: A34929
A;Molecule type: mRNA
A;Residues: 1-382 <KON>
A;Cross-references: GB:J05180; NID:g214821; PIDN:AAA49968.1; PID:g214822
R;Roberts, A.B.; Rosa, F.; Roche, N.S.; Coligan, J.E.; Garfield, M.; Rebbert, M.L.; Kondaiah, P.; Danielpour, D.; Kehrl, J.H.; Wahl, S.M.; Dawid, I.B.; Sporn, M.B.
Growth Factors 2, 135-147, 1990
A;Title: Isolation and characterization of TGF-beta2 and TGF-beta5 from medium conditioned by Xenopus XTC cells.
A;Reference number: A61036; MUID:90253806; PMID:2340184
A;Accession: B61036
A;Molecule type: protein
A;Residues: 271-276, 'X', 278-284, 'XX', 287-299 <ROB>
C;Superfamily: inhibin
C;Keywords: growth factor
F;271-382/Product: transforming growth factor beta-5 #status experimental <MAT>

Query Match 40.9%; Score 887.5; DB 2; Length 382;
Best Local Similarity 46.4%; Pred. No. 4.8e-64;
Matches 192; Conservative 54; Mismatches 121; Indels 47; Gaps 11;

```

Qy      9 LPLLLPLLWLLVLTGPRPAAGLSTCKTIDMELVKRKRIEAIHQILSKLRLASPPSQGDV 68
      : :| || |||| | |||| :||| |::||| ||||| ||||| :| | |
Db      1 MEVLWMLLVLLVHLSSLAMSLSTCKAVDMEEVRKRRIEAIHQILSKLKLDKTPDV-DS 59

Qy     69 PPGPLPEAVLALYNSTRDRVAGESVEPE-----PEPEADYYAKEVTRVLMVESGNQIYDK 123
      :| : ||||| : : : : | : ||||| :| | || : : |
Db     60 EKMTVPSEAIFLYNSTLEVIREKATREEEHVGHQDNIQDYAKQVYR---FESITELED- 115

Qy    124 FKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKL--KVEQHVELYQKYSNDSW-- 179
      | || | :|| | || |||| : : : : :| :|| :| :
Db    116 -----HEFKFKFNASHVRENVGMNSLLHHAELRMYKKQTDKNMDQRMELFWKYQENGTT 170

Qy    180 -RYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHCSC---DSKDNTHLVE 235
      ||| : : | ||:|||| | :|| | | | | | | :|| : :
Db    171 SRYLESKYITPVTDDWMSFDVTKTVNEWLKRAEBENEQFGLQPACKCPTQAKD----ID 226

Qy    236 INGFNSGRRGDLATIHGM--NRPFLLLMATPLERAQHLHSSRRHRRALDTNSYPYDVPDYA 293
      | || ||||| : : :| :| : : | || : ||| :|
Db    227 IEGF-PALRGDLASLSSKENTKPYLMTSMPAERIDTVTSSRKKR----- 270

Qy    294 SLALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQY 353
      : ||| : |||| : ||| : ||||| ||||| ||||| ||||| :||| :|||
Db    271 --GVGQEYCFGNGNPCCVKPLYINFRKDLGWKWIHEPKGYEANYCLGNCPIYWSMDTQY 328

Qy    354 SKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
      |||| :||| :||| :||| ||||| :||| ||||| :||| ||
Db    329 SKVLSLYNQNNPGASISPCCVPDVLEPLPIIYYVGRTAKVEQLSNMVVRSCNCS 382

```

RESULT 13

S01825

transforming growth factor beta-3 precursor - pig

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jul-1999

C;Accession: S01825
R;Derynck, R.; Lindquist, P.B.; Lee, A.; Wen, D.; Tamm, J.; Graycar, J.L.; Rhee, L.; Mason, A.J.; Miller, D.A.; Coffey, R.J.; Moses, H.L.; Chen, E.Y.
EMBO J. 7, 3737-3743, 1988
A;Title: A new type of transforming growth factor-beta, TGF-beta3.
A;Reference number: S01824; MUID:89091120; PMID:3208746
A;Accession: S01825
A;Molecule type: mRNA
A;Residues: 1-409 <DER>
A;Cross-references: EMBL:X14150; NID:g2127; PIDN:CAA32363.1; PID:g2128
C;Superfamily: inhibin
C;Keywords: growth factor
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-297/Domain: propeptide #status predicted <PRO>
F;298-409/Product: transforming growth factor beta-3 #status predicted <MAT>

Query Match 39.2%; Score 851; DB 2; Length 409;
Best Local Similarity 44.6%; Pred. No. 4.8e-61;
Matches 190; Conservative 58; Mismatches 122; Indels 56; Gaps 13;

```

Qy      15 LLWLLVLTTPGRPAAGLSTCKTIDMELVKRKRIEAI RQILSKLRLASPPSQGDVPPGGLP 74
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      7 LVVLALLNFATVSLMSMSTCTTLD F DHIK RKRVEAIRQILSKLRLTSPDP SML--ANIP 64

Qy      75 EAVLALYNSTR---DRVAGESVE--PEPEPEADYYAKEVTRVLMV---ESGNQIYDKFKG 126
      || ||||| : | || : : | : ||||| : : | : | : | : ||
Db      65 TQVLDLYNSTRELLEEVHGERGDDCTQENT ESEYYAKEIYKFDMIQGLEEHNDLAVCPKG 124

Qy      127 TPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL----KLKVEQHVELYQKYSND----S 178
      : : || | : : | || | : || : : | : | : | : | : |
Db      125 ITSKI FR-FNVSSVEK---NETNLFRAEFRVLRMPNPSSKRSEQRIELFQILQPDEHIAK 180

Qy      179 WRYLSNRL LAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHCSC-----DSK 228
      || : : | : ||||| || : || || : | : | || | : :
Db      181 QRYIDGKNLPTRGAAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNGDILENI 240

Qy      229 DNTLHVEINGFNS---GRRGDLATIHGM--NRPFLLLMATPLERAQH--LHSSRHRRALD 281
      : : : | : | ||| : : | : || | : | : | : | : |
Db      241 QEVMEIKFKGVDS EDDPGRGDLGRLKKKKEHSPHLILMMI PPDRLDNPG LGAQ RKKR--- 297

Qy      282 TNSYPYDVDPDYASLALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLG 341
      ||||| : | : ||| ||||| : ||||| : ||||| : ||| |
Db      298 -----ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWWHEPKGYANFCSG 343

Qy      342 PCPYIWSLDTQYSKVLALYNQHNP GASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIV 401
      ||| : | || : | || || || ||| : ||||| ||| : ||||| ||||| : |
Db      344 PCPYLRSADTT HSSVLGLYNTLNPEASASPCVPQDLEPLTILYYVGR TAKVEQLSNMVV 403

Qy      402 RSCKCS 407
      : |||||
Db      404 KSCKCS 409

```

RESULT 14
A41397
transforming growth factor beta-3 precursor - mouse
C;Species: Mus musculus (house mouse)


```

QY      229 DNTLHVEINGFNS---GRRGDLATIHGM---NRPFLLLMATPLERAQHLHSSRHRRALDT 282
      : :: | :: ||| : : | :| | | | :
Db      241 HEVMEIKFKGVDNEDDHGRGDLGRLKKQKDHHNPHLIILMMI PPHRLDSPGQGSQRK---- 296

QY      283 NSYPYDVPDYASLALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGP 342
      ||||| : |:||| |||||:|||||:|||||:||||| ||
Db      297 -----KRALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWWHEPKGYANFCSGP 345

QY      343 CPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYVGRKPKVEQLSNMIVR 402
      |||: | || :| || || | |||:||||| ||| |:||| | |||||:|:
Db      346 CPYLRADTTHSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVK 405

QY      403 SCKCS 407
      |||||
Db      406 SCKCS 410

```

RESULT 15

WFMSB2

transforming growth factor beta-2 precursor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 18-Jun-1999

C;Accession: A40148

R;Miller, D.A.; Lee, A.; Pelton, R.W.; Chen, E.Y.; Moses, H.L.; Derynck, R.

Mol. Endocrinol. 3, 1108-1114, 1989

A;Title: Murine transforming growth factor-beta2 cDNA sequence and expression in adult tissues and embryos.

A;Reference number: A40148; MUID:90014832; PMID:2797004

A;Accession: A40148

A;Molecule type: mRNA

A;Residues: 1-414 <MIL>

A;Cross-references: EMBL:X57413; NID:g54772; PIDN:CAA40672.1; PID:g54773

C;Comment: None of the three predicted glycosylation sites is in the mature protein.

C;Superfamily: inhibin

C;Keywords: glycoprotein; growth factor; growth regulation; homodimer; mitogen

F;1-19/Domain: signal sequence #status predicted <SIG>

F;20-302/Domain: propeptide #status predicted <PRO>

F;303-414/Product: transforming growth factor beta-2 #status predicted <MAT>

F;72,140,241/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 38.9%; Score 844; DB 1; Length 414;

Best Local Similarity 44.0%; Pred. No. 1.8e-60;

Matches 191; Conservative 61; Mismatches 120; Indels 62; Gaps 15;

```

QY      12 LLPLLWLLVLTPGRPAAGLSTCKTIDMELVKKRKRIEAI RQILSKLRLASPPSQGDVP-P 70
      :| || | | | |||| |::| : ||||| |||||:| ||| | | |
Db      5 VLSTFLLLHLVP--VALSLSTCSTLDMDQFMRKRIEAI RQILSKLKLTSPP--DYEP 60

QY      71 GPLPEAVLALYNSTRD---RVAGESVEPEPE-PEADYYAKEVTRVLM---VESGNQIYD 122
      :| |::| ||||| : : : | | | :||| ||| :| : | | |
Db      61 DEVPPVISIYNSTRDLLQEKASRRAAACERERSEQEYYAKEVYKIDMPSHLPSENAIPP 120

QY      123 KFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL---KLKV-EQHVELYQ-----K 173
      | | : : | : : | :| | :| | | :| | | :|||
Db      121 TFY-RPYFRIVRFDVSTMEKNASN---LVKAEFRVFRLLQNP KARVAEQRIELYQILKSKD 176

```



```

Qy      174 YSNDSWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHCSC----- 225
      : : | : : : : | | | | | | | | : : | : : | | | |
Db      177 LTSPTQRYIDSKVVKTRAEGEWLSFDVTDVQEWLHHKDRNLGFKISLHCPCTFVPSNN 236

Qy      226 ---DSKDNTLHVE---INGFNSGRRGDLATIHGMNR-----PFLLLMATPLERAQHLHS 273
      : | | | | : | : : | | | | : | | | | | | : |
Db      237 YIIPNKSEELERFAGIDGTSTYASGDQKTIKSTRKKTSGKTPHLLLMLLPSYRLESQQS 296

Qy      274 SRHRRALDTNSYPYDVPDYASLALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKG 333
      | | : : | | | | | | : : | | | | | | | | | | | |
Db      297 SRRKKR-----ALDAAYCFRNVQDNCCLRPLYIDFKRDLGWKWIHEPKG 340

Qy      334 YHANFCLGPCPYIWSLDTQYSKVLALYNQHNPASAAPCCVPQALEPLPIVYYVGRKPKV 393
      | : | | | | | | : | | | : | | : | | | | | | | | : | | : | | :
Db      341 YNANFCAGACPYLWSSDTQHTKVLSLYNTINPEASAPCCVSDLEPLTILYYIGNTPKI 400

Qy      394 EQLSNMIVRSCKCS 407
      | | | | | | : | | | |
Db      401 EQLSNMIVKSKCS 414

```

Search completed: October 28, 2003, 09:09:50
Job time : 14.4491 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 28, 2003, 00:08:41 ; Search time 8.15764 Seconds
(without alignments)
2346.251 Million cell updates/sec

Title: US-10-017-372E-39
Perfect score: 2169
Sequence: 1 MAPSGLRLLPLLLPLLWLLV.....GRKPKVEQLSNMIVRSCKCS 407

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	2050.5	94.5	390	1	TGF1_PIG	P07200	sus scrofa
2	1949.5	89.9	390	1	TGF1_SHEEP	P50414	ovis aries
3	1936.5	89.3	390	1	TGF1_HUMAN	P01137	homo sapien
4	1934.5	89.2	390	1	TGF1_CERAE	P09533	cercopithec
5	1913.5	88.2	390	1	TGF1_CANFA	P54831	canis famil
6	1859.5	85.7	390	1	TGF1_HORSE	O19011	equus cabal
7	1855.5	85.5	390	1	TGF1_MOUSE	P04202	mus musculu
8	1855.5	85.5	390	1	TGF1_RAT	P17246	rattus norv
9	1846.5	85.1	390	1	TGF1_CAVPO	Q9zly6	cavia porce
10	1592.5	73.4	315	1	TGF1_BOVIN	P18341	bos taurus
11	1067	49.2	373	1	TGF1_CHICK	P09531	gallus gall
12	887.5	40.9	382	1	TGF1_XENLA	P16176	xenopus lae
13	869.5	40.1	412	1	TGF3_CHICK	P16047	gallus gall
14	851	39.2	409	1	TGF3_PIG	P15203	sus scrofa
15	844.5	38.9	410	1	TGF3_MOUSE	P17125	mus musculu
16	844	38.9	414	1	TGF2_MOUSE	P27090	mus musculu
17	843.5	38.9	412	1	TGF3_RAT	Q07258	rattus norv
18	841.5	38.8	412	1	TGF3_HUMAN	P10600	homo sapien
19	829	38.2	414	1	TGF2_HUMAN	P08112	homo sapien
20	828.5	38.2	413	1	TGF2_XENLA	P17247	xenopus lae
21	825	38.0	412	1	TGF2_CHICK	P30371	gallus gall
22	825	38.0	435	1	TGF2_PIG	P09858	sus scrofa
23	825	38.0	442	1	TGF2_RAT	Q07257	rattus norv
24	482	22.2	112	1	TGF2_BOVIN	P21214	bos taurus
25	323.5	14.9	375	1	GDF8_MELGA	O42221	meleagris g
26	321.5	14.8	375	1	GDF8_CHICK	O42220	gallus gall
27	312.5	14.4	375	1	GDF8_PIG	O18831	sus scrofa
28	311.5	14.4	375	1	GDF8_PAPHA	O18828	papio hamad
29	309.5	14.3	376	1	GDF8_RAT	O35312	rattus norv
30	308.5	14.2	375	1	GDF8_HUMAN	O14793	homo sapien
31	307.5	14.2	376	1	GDF8_MOUSE	O08689	mus musculu
32	305.5	14.1	375	1	GDF8_SHEEP	O18830	ovis aries
33	298	13.7	405	1	GDFB_MOUSE	Q9z1w4	mus musculu
34	298	13.7	407	1	GDFB_HUMAN	O95390	homo sapien
35	296.5	13.7	375	1	GDF8_BOVIN	O18836	bos taurus
36	280.5	12.9	374	1	GDF8_BRARE	O42222	brachydanio
37	276.5	12.7	345	1	GDFB_RAT	Q9z217	rattus norv
38	275	12.7	425	1	IHBA_SHEEP	P43032	ovis aries
39	271.5	12.5	426	1	IHBA_HORSE	P55102	equus cabal
40	270.5	12.5	424	1	IHBA_PIG	P03970	sus scrofa
41	270	12.4	425	1	IHBA_BOVIN	P07995	bos taurus
42	268.5	12.4	424	1	IHBA_MOUSE	Q04998	mus musculu
43	268.5	12.4	424	1	IHBA_RAT	P18331	rattus norv
44	265.5	12.2	424	1	IHBA_CHICK	P27092	gallus gall
45	263	12.1	424	1	BM10_HUMAN	O95393	homo sapien

ALIGNMENTS

TGF1_PIG

ID TGF1_PIG STANDARD; PRT; 390 AA.

AC P07200; P08832;

DT 01-APR-1988 (Rel. 07, Created)

DT 01-APR-1988 (Rel. 07, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Transforming growth factor beta 1 precursor (TGF-beta 1).

GN TGFB1.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Ovary;

RX MEDLINE=87174844; PubMed=3470708;

RA Derynck R., Rhee L.;

RT "Sequence of the porcine transforming growth factor-beta precursor.";

RL Nucleic Acids Res. 15:3187-3187(1987).

RN [2]

RP SEQUENCE FROM N.A., AND VARIANT VAL-114.

RC STRAIN=Miniature swine;

RX MEDLINE=89054010; PubMed=2461367;

RA Kondaiah P., van Obberghen-Schilling E., Ludwig R.L., Dhar R.,

RA Sporn M.B., Roberts A.B.;

RT "cDNA cloning of porcine transforming growth factor-beta 1 mRNAs.

RT Evidence for alternate splicing and polyadenylation.";

RL J. Biol. Chem. 263:18313-18317(1988).

RN [3]

RP SEQUENCE FROM N.A., AND VARIANT VAL-114.

RX MEDLINE=88335639; PubMed=3166520;

RA Jakowlew S.B., Dillard P.J., Sporn M.B., Roberts A.B.;

RT "Nucleotide sequence of chicken transforming growth factor-beta 1

RT (TGF-beta 1).";

RL Nucleic Acids Res. 16:8730-8730(1988).

RN [4]

RP SHOWS THAT REF.3 SEQUENCE IS FROM PIG.

RA Jakowlew S.B.;

RL Unpublished observations (MAR-1996).

RN [5]

RP SEQUENCE FROM N.A., AND VARIANT VAL-114.

RA Wimmers K., Chomdej S., Ponsuksili S., Schellander K.;

RT "Polymorphism in the porcine transforming growth factor beta 1

RT gene.";

RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

RN [6]

RP SEQUENCE OF 279-322.

RX MEDLINE=87102890; PubMed=2879635;

RA Cheifetz S., Weatherbee J.A., Tsang M.L.S., Anderson J.K., Mole J.E.,

RA Lucas R., Massague J.;

RT "The transforming growth factor-beta system, a complex pattern of

RT cross-reactive ligands and receptors.";

RL Cell 48:409-415(1987).

CC -!- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL

CC PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL

CC TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM

CC HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE

CC ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
 CC A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
 CC -!- SUBUNIT: Homodimer; disulfide-linked.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the TGF-beta family.
 CC -!- CAUTION: REF.3 SEQUENCE WHICH WAS SAID TO ORIGINATE FROM CHICKEN
 CC WHITE LEGHORN, SEEMS (REF.4) TO ORIGINATE FROM PIG.
 CC -----
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 CC -----
 DR EMBL; Y00111; CAA68291.1; -.
 DR EMBL; M23703; AAA64616.1; -.
 DR EMBL; X12373; CAA30933.1; -.
 DR EMBL; AF461808; AAL57902.1; -.
 DR PIR; A27512; A27512.
 DR HSSP; P01137; 1KLA.
 DR InterPro; IPR002400; GF_cysknot.
 DR InterPro; IPR003911; TGF_TGFb.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR PRINTS; PR00438; GFCYSKNOT.
 DR PRINTS; PR01423; TGFBETA.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFB; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Growth factor; Mitogen; Glycoprotein; Signal; Polymorphism.
 FT SIGNAL 1 23 POTENTIAL.
 FT PROPEP 24 278
 FT CHAIN 279 390 TRANSFORMING GROWTH FACTOR BETA 1.
 FT DISULFID 285 294 BY SIMILARITY.
 FT DISULFID 293 356 BY SIMILARITY.
 FT DISULFID 322 387 BY SIMILARITY.
 FT DISULFID 326 389 BY SIMILARITY.
 FT DISULFID 355 355 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 82 82 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SITE 244 246 CELL ATTACHMENT SITE (POTENTIAL).
 FT VARIANT 114 114 L -> V.
 FT CONFLICT 6 7 LR -> PG (IN REF. 3).
 FT CONFLICT 180 180 R -> G (IN REF. 3).
 FT CONFLICT 237 237 N -> NA (IN REF. 3).
 SQ SEQUENCE 390 AA; 44294 MW; A6E2C3659FC384E6 CRC64;

Query Match 94.5%; Score 2050.5; DB 1; Length 390;
 Best Local Similarity 95.3%; Pred. No. 6.5e-157;
 Matches 388; Conservative 1; Mismatches 1; Indels 17; Gaps 1;

Qy 1 MAPSGLRLLPLLLPLLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAI RQGILSKLR L A 60

Db	1	MPPSGLRLLPLLLPLLLVLTTPGRPAAGLSTCKTIDMELVVRKRIEAIKRGQILSKRLRA	60
QY	61	SPPSQGDVPPGGLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI	120
Db	61	SPPSQGDVPPGGLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMLESQGNQI	120
QY	121	YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR	180
Db	121	YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR	180
QY	181	YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAI EGFRLSAHCSCDSKDNTHVEINGFN	240
Db	181	YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAI EGFRLSAHCSCDSKDNTHVEINGFN	240
QY	241	SGRRGDLATI HGMNRPFLLLMATPLERAQHLHSSRHRRALDNTSYPDVPDYASLALDTN	300
Db	241	SGRRGDLATI HGMNRPFLLLMATPLERAQHLHSSRHRR-----ALDTN	283
QY	301	YCFSSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY	360
Db	284	YCFSSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY	343
QY	361	NQHNP GASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS	407
Db	344	NOHNP GASAAPCCVPOALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS	390

RESULT 2

TGF1 SHEEP

ID TGF1 SHEEP STANDARD; PRT; 390 AA.

AC P50414;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Transforming growth factor beta 1 precursor (TGF-beta 1).

GN TGFB1.

OS Ovis aries (Sheep).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea:

OC Bovidae; Caprinae; Ovis.

OX NCBI TaxID=9940;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=95121932; PubMed=7821809;

RA Woodall C.J., McLaren L.J., Watt N.J.;

RT "Sequence and chromosomal localisation of the gene encoding ovine
RT latent transforming growth factor-beta 1.";

RL Gene 150:371-373 (1994).

RN [2]

RP SEQUENCE OF 281-390 FROM N.A.

RC STRAIN=Merino; TISSUE=Skin;

RX MEDLINE=95268698; PubMed=7749621;

RA Sutton R., Ward W.G., Raphael K.A., Cam G.R.;

RT "Growth factor expression in skin during wool follicle development.";

RL Comp. Biochem. Physiol. 110B:697-705 (1995).

CC -!- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL

CC PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
CC HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
CC ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
CC A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.

CC -!- SUBUNIT: Homodimer; disulfide-linked.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the TGF-beta family.

```

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CC -----

DR EMBL; X76916; CAA54242.1; -.

DR EMBL; L36038; AAA31526.1; -.

DR PIR: I46463; I46463.

DR HSSP: P01137: 1KLA.

DR InterPro; IPR002400; GF cysknot.

DR InterPro; IPR003911; TGF TGFb.

DR InterPro; IPR001839; TGFb.

DR InterPro; IPR001111; TGFb N.

DR Pfam; PF00019; TGF-beta; 1.

DR Pfam; PF00688; TGFb propeptide; 1.

DR PRINTS; PR00438; GFCYSKNOT.

DR PRINTS; PR01423; TGFBETA.

DR ProDom; PD000357; TGFb; 1.

DR SMART; SM00204; TGFB; 1.

DR PROSITE; PS00250; TGF BETA 1; 1.

KW Growth factor; Mitogen; Glycoprotein; Signal.

FT	SIGNAL	1	23	POTENTIAL.
----	--------	---	----	------------

FT PROPEP 24 278 POTENTIAL.

FT CHAIN 279 390 TRANSFORMING GROWTH FACTOR BETA 1.

FT DISULFID 285 294 BY SIMILARITY.

FT DISULFID 293 356 BY SIMILARITY.

FT	DISULFID	322	387	BY SIMILARITY.
----	----------	-----	-----	----------------

FT DISULFID 326 389 BY SIMILARITY.

FT	DISULFID	355	355	INTERCHAIN (BY SIMILARITY).
----	----------	-----	-----	-----------------------------

FT	CARBOHYD	82	82	N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT	CARBOHYD	136	136	N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT	CARBOHYD	176	176	N-LINKED (GLCNAC. . .) (POTENTIAL).
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FT	SITE	244	246	CELL ATTACHMENT SITE (POTENTIAL).
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SQ SEQUENCE 390 AA; 44291 MW; 1C247299484D0E57 CRC64;

Query Match 89.9%; Score 1949.5; DB 1; Length 390;

Best Local Similarity 90.2%; Pred. No. 8.1e-149;

Matches 367; Conservative 10; Mismatches 13; Indels 17; Gaps 1;

QY 1 MAPSGRLRLLPLLLPLLWLLVLTGPRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
| | | | | : | | | | |

Db 1 MPPSGLRLLPLLLPLLWLLMLTPGRPVLGLSTCKTIDMELVKRKGIEAIRGOILSKLRLA 60

Qy 61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
| | | | | | | | | | : | | | | | | | | | | | | | | | | | | | | | | : |

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Db          61 SPSPQGDVPPGPLPEAILALYNSTRDRVAGESAETEPEPEADYYAKEVTRVLMVEYGNKI 120
Qy          121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
          ||| | : ||:| | ||||| ||||| ||||| : ||||| ||||| ||||| : |||
Db          121 YDKMKSSSHSIYMFFNTSELREAVPEPVLLSRADVRLRLKLKVEQHVELYQKYSNNSWR 180
Qy          181 YLSNRL LAPSDSPEWLSFDVTGVVRQWLTRREAI EGFRLSAHCSCDSKDNTLHVEINGFN 240
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : ||||| :
Db          181 YLSNRL LAPSDSPEWLSFDVTGVVRQWLTHREEI EGFRLSAHCSCDSKDNTLQVDINGFS 240
Qy          241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNSYPYDVPDYASLALDTN 300
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db          241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRR-----ALDTN 283
Qy          301 YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 360
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db          284 YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 343
Qy          361 NQHNP GASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db          344 NQHNP GASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390

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RESULT 3

TGF1_HUMAN

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ID   TGF1_HUMAN      STANDARD;          PRT;   390 AA.
AC   P01137; Q9UCG4;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-FEB-1991 (Rel. 17, Last sequence update)
DT   15-SEP-2003 (Rel. 42, Last annotation update)
DE   Transforming growth factor beta 1 precursor (TGF-beta 1).
GN   TGFB1 OR TGFB.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=87174845; PubMed=3470709;
RA   Derynck R., Rhee L., Chen E.Y., van Tilburg A.;
RT   "Intron-exon structure of the human transforming growth factor-beta
RT   precursor gene.";
RL   Nucleic Acids Res. 15:3188-3189(1987).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85296301; PubMed=3861940;
RA   Derynck R., Jarrett J.A., Chen E.Y., Eaton D.H., Bell J.R.,
RA   Assoian R.K., Roberts A.B., Sporn M.B., Goeddel D.V.;
RT   "Human transforming growth factor-beta complementary DNA sequence and
RT   expression in normal and transformed cells.";
RL   Nature 316:701-705(1985).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Duodenum, and Eye;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

```

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP SEQUENCE OF 279-390 FROM N.A.
 RC TISSUE=Carcinoma;
 RA Urushizaki Y., Niitsu Y., Terui T., Koshida Y., Mahara K., Kohgo Y.,
 RA Urushizaki I., Takahashi Y., Ito H.;
 RT "Cloning and expression of the gene for human transforming growth
 RT factor-beta in Escherichia coli.";
 RL Tumor Res. 22:41-55(1987).
 RN [5]
 RP SEQUENCE OF 279-329.
 RC TISSUE=Bladder carcinoma;
 RX MEDLINE=93229900; PubMed=8471846;
 RA Bourdrel L., Lin C.-H., Lauren S.L., Elmore R.H., Sugarman B.J.,
 RA Hu S., Westcott K.R.;
 RT "Recombinant human transforming growth factor-beta 1: expression by
 RT Chinese hamster ovary cells, isolation, and characterization.";
 RL Protein Expr. Purif. 4:130-140(1993).
 RN [6]
 RP SEQUENCE OF 279-301.
 RX MEDLINE=85131019; PubMed=2982829;
 RA Massague J., Like B.;
 RT "Cellular receptors for type beta transforming growth factor. Ligand
 RT binding and affinity labeling in human and rodent cell lines.";
 RL J. Biol. Chem. 260:2636-2645(1985).
 RN [7]
 RP STRUCTURE BY NMR OF 279-390.
 RX MEDLINE=93144319; PubMed=8424942;
 RA Archer S.J., Bax A., Roberts A.B., Sporn M.B., Ogawa Y., Piez K.A.,
 RA Weatherbee J.A., Tsang M.L.-S., Lucas R., Zheng B.-L., Wenker J.,
 RA Torchia D.A.;
 RT "Transforming growth factor beta 1: NMR signal assignments of the
 RT recombinant protein expressed and isotopically enriched using Chinese
 RT hamster ovary cells.";
 RL Biochemistry 32:1152-1163(1993).
 RN [8]
 RP STRUCTURE BY NMR OF 279-390.
 RX MEDLINE=93144320; PubMed=8424943;
 RA Archer S.J., Bax A., Roberts A.B., Sporn M.B., Ogawa Y., Piez K.A.,
 RA Weatherbee J.A., Tsang M.L.-S., Lucas R., Zheng B.-L., Wenker J.,

RA Torchia D.A.;
 RT "Transforming growth factor beta 1: secondary structure as determined
 RT by heteronuclear magnetic resonance spectroscopy.";
 RL Biochemistry 32:1164-1171(1993).
 RN [9]
 RP STRUCTURE BY NMR OF 279-390.
 RX MEDLINE=96266150; PubMed=8679613;
 RA Hinck A.P., Archer S.J., Qian S.W., Roberts A.B., Sporn M.B.,
 RA Weatherbee J.A., Tsang M.L.-S., Lucas R., Zheng B.-L., Wenker J.,
 RA Torchia D.A.;
 RT "Transforming growth factor beta 1: three-dimensional structure in
 RT solution and comparison with the X-ray structure of transforming
 RT growth factor beta 2.";
 RL Biochemistry 35:8517-8534(1996).
 CC -!- FUNCTION: MULTIFUNCTIONAL PEPTIDE THAT CONTROLS PROLIFERATION,
 CC DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL TYPES. MANY
 CC CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF THEM HAVE
 CC SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1 REGULATES THE
 CC ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES A
 CC POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
 CC -!- SUBUNIT: Homodimer; disulfide-linked.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the TGF-beta family.
 CC -----
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 CC -----
 DR EMBL; X05839; CAA29283.1; -.
 DR EMBL; X05840; CAA29283.1; JOINED.
 DR EMBL; X05843; CAA29283.1; JOINED.
 DR EMBL; X05844; CAA29283.1; JOINED.
 DR EMBL; X05849; CAA29283.1; JOINED.
 DR EMBL; X05850; CAA29283.1; JOINED.
 DR EMBL; X02812; CAA26580.1; ALT_SEQ.
 DR EMBL; BC001180; AAH01180.1; -.
 DR EMBL; BC000125; AAH00125.1; -.
 DR EMBL; BC022242; AAH22242.1; -.
 DR EMBL; M38449; AAA36735.1; -.
 DR PIR; A27513; WFHU2.
 DR PDB; 1KLA; 17-AUG-96.
 DR PDB; 1KLC; 17-AUG-96.
 DR PDB; 1KLD; 17-AUG-96.
 DR Genew; HGNC:11766; TGFB1.
 DR MIM; 190180; -.
 DR GO; GO:0006916; P:anti-apoptosis; TAS.
 DR InterPro; IPR002400; GF_cysknot.
 DR InterPro; IPR003911; TGF_TGfb.
 DR InterPro; IPR001839; TGfb.
 DR InterPro; IPR001111; TGfb_N.
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGfb_propeptide; 1.
 DR PRINTS; PR00438; GFCYSKNOT.

```

DR PRINTS; PR01423; TGFbeta.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor; Mitogen; Glycoprotein; Signal; 3D-structure.
FT SIGNAL 1 23 POTENTIAL.
FT PROPEP 24 278
FT CHAIN 279 390 TRANSFORMING GROWTH FACTOR BETA 1.
FT DISULFID 285 294
FT DISULFID 293 356
FT DISULFID 322 387
FT DISULFID 326 389
FT DISULFID 355 355 INTERCHAIN.
FT CARBOHYD 82 82 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT SITE 244 246 CELL ATTACHMENT SITE (POTENTIAL).
FT CONFLICT 10 10 L -> P (IN REF. 2).
FT CONFLICT 159 159 R -> RR (IN REF. 2).
FT STRAND 281 281
FT TURN 282 287
FT STRAND 294 296
FT STRAND 300 300
FT TURN 302 305
FT STRAND 313 313
FT STRAND 317 317
FT STRAND 321 323
FT HELIX 335 346
FT TURN 348 349
FT STRAND 358 370
FT TURN 371 372
FT STRAND 373 387
SQ SEQUENCE 390 AA; 44341 MW; 75391614250288FE CRC64;

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[illegible]

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QY      301 YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 360
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Db      284 YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 343

QY      361 NQHNP GASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      344 NQHNP GASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390

```

RESULT 4

TGF1_CERAE

```

ID      TGF1_CERAE      STANDARD;      PRT;      390 AA.
AC      P09533;
DT      01-MAR-1989 (Rel. 10, Created)
DT      01-MAR-1989 (Rel. 10, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Transforming growth factor beta 1 precursor (TGF-beta 1).
GN      TGFB1.
OS      Cercopithecus aethiops (Green monkey) (Grivet).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC      Cercopithecinae; Cercopithecus.
OX      NCBI_TaxID=9534;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=87246074; PubMed=3474130;
RA      Sharples K., Plowman G.D., Rose T.M., Twardzik D.R., Purchio A.F.;
RT      "Cloning and sequence analysis of simian transforming growth
RT      factor-beta cDNA.";
RL      DNA 6:239-244(1987).
CC      -!- FUNCTION: MULTIFUNCTIONAL PEPTIDE THAT CONTROL PROLIFERATION,
CC      DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL TYPES. MANY
CC      CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM HAVE
CC      SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
CC      ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES A
CC      POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC      -!- SUBUNIT: Homodimer; disulfide-linked.
CC      -!- SUBCELLULAR LOCATION: Secreted.
CC      -!- SIMILARITY: Belongs to the TGF-beta family.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; M16658; AAA35369.1; -.
DR      PIR; A26960; A26960.
DR      HSSP; P01137; 1KLA.
DR      InterPro; IPR002400; GF_cysknot.
DR      InterPro; IPR003911; TGF_TGFB.
DR      InterPro; IPR001839; TGFB.
DR      InterPro; IPR001111; TGFB_N.
DR      Pfam; PF00019; TGF-beta; 1.

```

DR Pfam; PF00688; TGFb_propeptide; 1.
 DR PRINTS; PR00438; GFCYSKNOT.
 DR PRINTS; PR01423; TGFbeta.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFB; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Growth factor; Mitogen; Glycoprotein; Signal.
 FT SIGNAL 1 16 POTENTIAL.
 FT PROPEP 17 278
 FT CHAIN 279 390 TRANSFORMING GROWTH FACTOR BETA 1.
 FT DISULFID 285 294 BY SIMILARITY.
 FT DISULFID 293 356 BY SIMILARITY.
 FT DISULFID 322 387 BY SIMILARITY.
 FT DISULFID 326 389 BY SIMILARITY.
 FT DISULFID 355 355 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 82 82 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SITE 244 246 CELL ATTACHMENT SITE (POTENTIAL).
 SQ SEQUENCE 390 AA; 44356 MW; DFF63E2BAB44320E CRC64;

Query Match 89.2%; Score 1934.5; DB 1; Length 390;
 Best Local Similarity 89.9%; Pred. No. 1.3e-147;
 Matches 366; Conservative 10; Mismatches 14; Indels 17; Gaps 1;

Qy	1	MAPSGRLRLPLLLPLLWLLVLT	TPGRPAAGLSTCKTIDMELVKRKRIE	AIRGQILSKLRLA	60
Db	1	MPPSGRLRLPLLLPLLWLLVLT	TPSRPAAGLSTCKTIDMELVKRKRIE	TIRGQILSKLRLA	60
Qy	61	SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI	120		
		:			
Db	61	SPPSQGEVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVETHNEI	120		
		:			
Qy	121	YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR	180		
		:			
Db	121	YDKFKQSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNNSWR	180		
		:			
Qy	181	YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHCSCDSKDNTLHVEINGFN	240		
		:			
Db	181	YLSNRLLAPSNSPEWLSFDVTGVVRQWLSRGGEIEGFRLSAHCSCDSKDNTLQVDINGFT	240		
		:			
Qy	241	SGRRGDLATIHGMNRPFLLMATPLERAQHLHSSRRRALDTNSYPYDVPDYASLALDTN	300		
		:			
Db	241	TGRRGDLATIHGMNRPFLLMATPLERAQHLQSSRHRR-----ALDTN	283		
		:			
Qy	301	YCFSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY	360		
		:			
Db	284	YCFSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY	343		
		:			
Qy	361	NQHNPGASAAPCCVPQALEPLPIVYVGRKPKVEQLSNMIVRSCKCS	407		
		:			
Db	344	NQHNPGASAAPCCVPQALEPLPIVYVGRKPKVEQLSNMIVRSCKCS	390		
		:			

RESULT 5
 TGF1_CANFA
 ID TGF1_CANFA STANDARD; PRT; 390 AA.

AC P54831;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Transforming growth factor beta 1 precursor (TGF-beta 1).
GN TGFb1.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Jugular vein endothelial;
RX MEDLINE=95237630; PubMed=7721110;
RA Manning A.M., Auchampach J.A., Drong R.F., Slightom J.L.;
RT "Cloning of a canine cDNA homologous to the human transforming growth
RT factor-beta 1-encoding gene.";
RL Gene 155:307-308(1995).
CC -!- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
CC PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
CC HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
CC ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
CC A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC -!- SUBUNIT: Homodimer; disulfide-linked.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the TGF-beta family.
CC -----
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CC -----
DR EMBL; L34956; AAA51458.1; -.
DR PIR; JC4023; JC4023.
DR HSSP; P01137; 1KLA.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR003911; TGF_TGFb.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRINTS; PR01423; TGFbBETA.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor; Mitogen; Glycoprotein; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT PROPEP 24 278 BY SIMILARITY.
FT CHAIN 279 390 TRANSFORMING GROWTH FACTOR BETA 1.
FT DISULFID 285 294 BY SIMILARITY.
FT DISULFID 293 356 BY SIMILARITY.
FT DISULFID 322 387 BY SIMILARITY.


```

QY      61 SPSPQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 SPSPQGEVPPGPLPEAVLALYNSTRAQVAGESAETEPEPEADYYAKEVTRVLMVEKENEI 120

QY     121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLVQHVELYQKYSNDSWR 180
      | : ||:| ||||| |||:|:||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     121 YKTVETGSHSIYMFNTSELRAAVPDPMLLSRAELRLLRLKLSVEQHVELYQKYSNNSWR 180

QY     181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAI EGFRLSAHCSCDSKDNTLHVEINGFN 240
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     181 YLSNRLLTPSDSPEWLSFDVTGVVRQWLSQGGAMEGFRLSAHCSCDSKDNTLRVGINGFS 240

QY     241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRRHRRALDTNSYPYDVPDYASIALDTN 300
      | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     241 SSRRGDLATIDGMNRPFLLLMATPLERAQQLHSSRRHR-----ALDTN 283

QY     301 YCFSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 360
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     284 YCFSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 343

QY     361 NQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     344 NQHNPGASAAPCCVPQVLEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390

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RESULT 7

TGF1_MOUSE

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ID  TGF1_MOUSE      STANDARD;      PRT;      390 AA.
AC  P04202;
DT  20-MAR-1987 (Rel. 04, Created)
DT  20-MAR-1987 (Rel. 04, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Transforming growth factor beta 1 precursor (TGF-beta 1).
GN  TGFB1.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=86168129; PubMed=3007454;
RA  Derynck R., Jarrett J.A., Chen E.Y., Goeddel D.V.;
RT  "The murine transforming growth factor-beta precursor.";
RL  J. Biol. Chem. 261:4377-4379(1986).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=BALB/c;
RX  MEDLINE=96096545; PubMed=8522200;
RA  Guron C., Sudarshan C., Raghov R.;
RT  "Molecular organization of the gene encoding murine transforming
RT  growth factor beta 1.";
RL  Gene 165:325-326(1995).
RN  [3]
RP  SEQUENCE FROM N.A.
RC  STRAIN=C57BL/6, and NOD/LT; TISSUE=Spleen;
RA  Poirrot L., Benoist C., Mathis D.;

```



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RT  "Transforming growth factor-beta 1 sequence and expression: no
RT  difference between NOD/Lt and C57Bl/6 mouse strains.";
RL  Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
CC  -!- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
CC      PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC      TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
CC      HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
CC      ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
CC      A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC  -!- SUBUNIT: Homodimer; disulfide-linked.
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- SIMILARITY: Belongs to the TGF-beta family.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; M13177; AAA40423.1; -.
DR  EMBL; L42462; AAB00138.1; -.
DR  EMBL; L42456; AAB00138.1; JOINED.
DR  EMBL; L42457; AAB00138.1; JOINED.
DR  EMBL; L42458; AAB00138.1; JOINED.
DR  EMBL; L42459; AAB00138.1; JOINED.
DR  EMBL; L42460; AAB00138.1; JOINED.
DR  EMBL; L42461; AAB00138.1; JOINED.
DR  EMBL; AJ009862; CAA08900.1; -.
DR  PIR; A01396; WFMS2.
DR  HSSP; P01137; 1KLA.
DR  MGD; MGI:98725; Tgfb1.
DR  GO; GO:0005578; C:extracellular matrix; IDA.
DR  GO; GO:0006954; P:inflammatory response; IMP.
DR  GO; GO:0007515; P:lymph gland development; IMP.
DR  GO; GO:0008220; P:necrosis; IMP.
DR  GO; GO:0016202; P:regulation of myogenesis; IDA.
DR  InterPro; IPR002400; GF_cysknot.
DR  InterPro; IPR003911; TGF_TGfb.
DR  InterPro; IPR001839; TGfb.
DR  InterPro; IPR001111; TGfb_N.
DR  Pfam; PF00019; TGF-beta; 1.
DR  Pfam; PF00688; TGfb_propeptide; 1.
DR  PRINTS; PR00438; GFCYSKNOT.
DR  PRINTS; PR01423; TGFBETA.
DR  ProDom; PD000357; TGfb; 1.
DR  SMART; SM00204; TGFB; 1.
DR  PROSITE; PS00250; TGF_BETA_1; 1.
KW  Growth factor; Mitogen; Glycoprotein; Signal.
FT  SIGNAL          1      23      POTENTIAL.
FT  PROPEP          24      278
FT  CHAIN           279      390      TRANSFORMING GROWTH FACTOR BETA 1.
FT  DISULFID        285      294      BY SIMILARITY.
FT  DISULFID        293      356      BY SIMILARITY.
FT  DISULFID        322      387      BY SIMILARITY.
FT  DISULFID        326      389      BY SIMILARITY.

```

FT DISULFID 355 355 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 82 82 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 176 176 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SITE 244 246 CELL ATTACHMENT SITE (POTENTIAL).
 SQ SEQUENCE 390 AA; 44310 MW; 4381A51B711D689E CRC64;

Query Match 85.5%; Score 1855.5; DB 1; Length 390;
 Best Local Similarity 85.5%; Pred. No. 2.8e-141;
 Matches 348; Conservative 15; Mismatches 27; Indels 17; Gaps 1;

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Qy      1 MAPSGLRLLPLLLPLWLLVLTTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1 MPPSGLRLLPLLLPLPWLLVLTTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60

Qy     61 SPSPQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
      | | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     61 SPSPQGEVPPGPLPEAVLALYNSTRDRVAGESADPEPEPEADYYAKEVTRVLMVDRNNAI 120

Qy    121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLVKVEQHVELYQKYSNDSWR 180
      | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    121 YEKTKDISHSIYMFNTSDIREAVPEPPLLSRAELRLQRLKSSVEQHVELYQKYSNNSWR 180

Qy    181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHCSCDSKDNTLHVEINGFN 240
      | | | | | | : | : | | | | | | | | | | | | | | | | | | | | | |
Db    181 YLGNRLLTPTDTPWLSFDVTGVVRQWLNQGDGIQGFRFSAHCSCDSKDNKLHVEINGIS 240

Qy    241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNSYPYDVPDYASLALDTN 300
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    241 PKRRGDLGTIHDMNRPFLLLMATPLERAQHLHSSRHRR-----ALDTN 283

Qy    301 YCFSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 360
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    284 YCFSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 343

Qy    361 NQHNPASAAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
      | | | | | | | | : | | | | | | | | | | | | | | | | | | | | |
Db    344 NQHNPASASPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390
  
```

RESULT 8

TGF1_RAT
 ID TGF1_RAT STANDARD; PRT; 390 AA.
 AC P17246;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Transforming growth factor beta 1 precursor (TGF-beta 1).
 GN TGFB1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Heart;
 RX MEDLINE=90272425; PubMed=2349108;


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Qy      61 SPSPQGDVPPGGLPEAVLALYNSTRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQI 120
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 SPSPQGEVPPGGLPEAVLALYNSTRDRVAGESADPEPEPEADYYAKEVTRVLMVDRNNAI 120

Qy     121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
      ||| | ||:| ||||:| ||||| ||||| ||||| ||||| |||||:|||
Db     121 YDKTKDITHSIYMFNTSDIREAVPEPPLLSRAELRLQRFKSTVEQHVELYQKYSNNSWR 180

Qy     181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHCSCDSKDNTLHVEINGFN 240
      || |||| | |:| ||||| ||||| : : | :||| ||||| ||||| ||||| :
Db     181 YLGNRLLTPTDTPEWLSFDVTGVVRQWLNQGDGIQGFRLSAHCSCDSKDNVLHVEINGIS 240

Qy     241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTSYPYDVPDYASLALDTN 300
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     241 PKRRGDLGTIHDNRPFLLLMATPLERAQHLHSSRHR-----ALDTN 283

Qy     301 YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 360
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     284 YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 343

Qy     361 NQHNP GASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
      ||||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db     344 NQHNP GASASPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 390

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RESULT 9

TGF1_CAVPO

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ID   TGF1_CAVPO      STANDARD;          PRT;   390 AA.
AC   Q9Z1Y6; Q9QZB3; Q9R148;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Transforming growth factor beta 1 precursor (TGF-beta 1).
GN   TGFB1.
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Hartley;
RA   Jeevan A., McMurray D.N., Yoshimura T.;
RT   "Guinea pig transforming growth factor-beta in peritoneal exudates
RT   after BCG vaccination.";
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 265-382 FROM N.A.
RX   MEDLINE=99144670; PubMed=10025978;
RA   Scaroza A.M., Ramsingh A.I., Wicher V., Wicher K.;
RT   "Spontaneous cytokine gene expression in normal guinea pig blood and
RT   tissues.";
RL   Cytokine 10:851-859(1998).
RN   [3]
RP   SEQUENCE OF 279-371 FROM N.A.
RC   STRAIN=Hartley; TISSUE=Trachea;
RA   Morishima Y., Uchida Y., Nomura A., Ishii Y., Sakamoto T.,

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RA  Sekizawa K.;
RT  "Guinea-pig transforming growth factor-beta expression in injured
RT  tracheal epithelium.";
RL  Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
CC  -!- FUNCTION: MULTIFUNCTIONAL PEPTIDE THAT CONTROLS PROLIFERATION,
CC      DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL TYPES. MANY
CC      CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF THEM HAVE
CC      SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1 REGULATES THE
CC      ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES A
CC      POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC  -!- SUBUNIT: Homodimer; disulfide-linked (By similarity).
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- SIMILARITY: Belongs to the TGF-beta family.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; AF191297; AAF02780.1; -.
DR  EMBL; AF097509; AAC83807.1; -.
DR  EMBL; AF169347; AAD49347.1; -.
DR  HSSP; P01137; 1KLA.
DR  InterPro; IPR002400; GF_cysknot.
DR  InterPro; IPR003911; TGF_TGFB.
DR  InterPro; IPR001839; TGFB.
DR  InterPro; IPR001111; TGFB_N.
DR  Pfam; PF00019; TGF-beta; 1.
DR  Pfam; PF00688; TGFB_propeptide; 1.
DR  PRINTS; PR00438; GFCYSKNOT.
DR  PRINTS; PR01423; TGFBETA.
DR  ProDom; PD000357; TGFB; 1.
DR  SMART; SM00204; TGFB; 1.
DR  PROSITE; PS00250; TGF_BETA_1; 1.
KW  Growth factor; Mitogen; Glycoprotein; Signal.
FT  SIGNAL          1      24      POTENTIAL.
FT  PROPEP          25     278      POTENTIAL.
FT  CHAIN           279     390      TRANSFORMING GROWTH FACTOR BETA 1.
FT  DISULFID        285     294      BY SIMILARITY.
FT  DISULFID        293     356      BY SIMILARITY.
FT  DISULFID        322     387      BY SIMILARITY.
FT  DISULFID        326     389      BY SIMILARITY.
FT  DISULFID        355     355      INTERCHAIN (BY SIMILARITY).
FT  CARBOHYD         82      82      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD        136     136      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD        176     176      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  SITE            244     246      CELL ATTACHMENT SITE (POTENTIAL).
FT  CONFLICT        279     279      G -> P (IN REF. 3).
FT  CONFLICT        286     286      F -> S (IN REF. 2).
FT  CONFLICT        309     309      K -> E (IN REF. 2).
FT  CONFLICT        322     322      C -> R (IN REF. 2).
FT  CONFLICT        350     350      A -> G (IN REF. 2).
SQ  SEQUENCE        390 AA;  44328 MW;  1539F849BA0C0FF1 CRC64;

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Query Match 85.1%; Score 1846.5; DB 1; Length 390;
 Best Local Similarity 85.3%; Pred. No. 1.5e-140;
 Matches 347; Conservative 15; Mismatches 28; Indels 17; Gaps 1;

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QY      1 MAPSGLRLLPLLLPLLWLLVLTTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1 MPPSRLRLLPLLLPLLWLLVLAPGRPASGLSTCKTIDMELVKRKRIEAIRGQILSKLRLA 60

QY     61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESVEPEPEPEPEADYYAKEVTRVLMVESGNQI 120
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     61 SPPSQGDVPPGPLPEAVLALYNSTRDRVAGESAEPEPEPEPEPDYYAKEVTRVLMVDNSHNI 120

QY    121 YDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWR 180
      | : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    121 YKSIETVAHSIYMFNTSELREAVPDPLLSRAELRMQRLKLNVEQHVELYQKYSNNSWR 180

QY    181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHCSCDSKDNTLHVEINGFN 240
      | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    181 YLSNQLLTPSDTPEWLSFDVTGVVRQWLSQGEELEGFRFSAHCSCDSKDNTLRVEINGIG 240

QY    241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNSYPYDVPDYASLALDTN 300
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    241 PKRRGDLAATHGMNRPFLLLMATPLERAQHLHSSRHR-----GLDTN 283

QY    301 YCFSSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 360
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    284 YCFSSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 343

QY    361 NQHNPASAAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    344 NQHNPASAAAPCCVPQALEPLPIVYYVGRKAKVEQLSNMIVRSCKCS 390
  
```

RESULT 10

TGF1_BOVIN

```

ID  TGF1_BOVIN      STANDARD;      PRT;   315 AA.
AC  P18341;
DT  01-NOV-1990 (Rel. 16, Created)
DT  01-NOV-1990 (Rel. 16, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Transforming growth factor beta 1 precursor (TGF-beta 1) (Fragment).
GN  TGFBI.
OS  Bos taurus (Bovine).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC  Bovidae; Bovinae; Bos.
OX  NCBI_TaxID=9913;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=91042552; PubMed=3153459;
RA  van Obberghen-Schilling E., Kondaiah P., Ludwig R.L., Sporn M.B.,
RA  Baker C.C.;
RT  "Complementary deoxyribonucleic acid cloning of bovine transforming
RT  growth factor-beta 1.";
RL  Mol. Endocrinol. 1:693-698(1987).
RN  [2]
RP  SUBUNITS.
  
```

RC TISSUE=Bone;
 RX MEDLINE=92129307; PubMed=1733936;
 RA Ogawa Y., Schmidt D.K., Dasch J.R., Chang R.J., Glaser C.B.;
 RT "Purification and characterization of transforming growth factor-beta
 RT 2.3 and -beta 1.2 heterodimers from bovine bone.";
 RL J. Biol. Chem. 267:2325-2328(1992).
 CC -!- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
 CC PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
 CC TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
 CC HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
 CC ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
 CC A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
 CC -!- SUBUNIT: Homodimer; disulfide-linked. Heterodimers of TGF-beta 1/2
 CC have been found in bone.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the TGF-beta family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M36271; AAA30778.1; -.
 DR PIR; A40057; A40057.
 DR HSSP; P01137; 1KLA.
 DR InterPro; IPR002400; GF_cysknot.
 DR InterPro; IPR003911; TGF_TGFb.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb_N.
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR PRINTS; PR00438; GFCYSKNOT.
 DR PRINTS; PR01423; TGFBETA.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFB; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Growth factor; Mitogen; Glycoprotein.
 FT NON_TER 1 1
 FT PROPEP <1 203
 FT CHAIN 204 315 TRANSFORMING GROWTH FACTOR BETA 1.
 FT DISULFID 210 219 BY SIMILARITY.
 FT DISULFID 218 281 BY SIMILARITY.
 FT DISULFID 247 312 BY SIMILARITY.
 FT DISULFID 251 314 BY SIMILARITY.
 FT DISULFID 280 280 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 7 7 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SITE 169 171 CELL ATTACHMENT SITE (POTENTIAL).
 SQ SEQUENCE 315 AA; 36269 MW; C2717A23D994E00E CRC64;

Query Match 73.4%; Score 1592.5; DB 1; Length 315;
 Best Local Similarity 89.5%; Pred. No. 2.5e-120;
 Matches 297; Conservative 9; Mismatches 9; Indels 17; Gaps 1;


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CC  -!- FUNCTION: TGF-BETA IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROL
CC      PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC      TYPES. MANY CELLS SYNTHESIZE TGF-BETA AND ESSENTIALLY ALL OF THEM
CC      HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA REGULATES THE
CC      ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND DETERMINES
CC      A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC  -!- SUBUNIT: Homodimer; disulfide-linked.
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- SIMILARITY: Belongs to the TGF-beta family.
CC  -----
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CC  use by non-profit institutions as long as its content is in no way
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; M31160; AAB05637.1; -.
DR  PIR; A41918; A41918.
DR  HSSP; P01137; 1KLA.
DR  InterPro; IPR003911; TGF_TGFB.
DR  InterPro; IPR001839; TGFB.
DR  InterPro; IPR001111; TGFB_N.
DR  Pfam; PF00019; TGF-beta; 1.
DR  Pfam; PF00688; TGFB_propeptide; 1.
DR  PRINTS; PR01423; TGFBETA.
DR  ProDom; PD000357; TGFB; 1.
DR  SMART; SM00204; TGFB; 1.
DR  PROSITE; PS00250; TGF_BETA_1; 1.
KW  Growth factor; Mitogen; Glycoprotein; Signal.
FT  NON_TER      1      1
FT  SIGNAL        <1      1      POTENTIAL.
FT  PROPEP        2      259     POTENTIAL.
FT  CHAIN         260     373     TRANSFORMING GROWTH FACTOR BETA 1.
FT  DISULFID      266     277     BY SIMILARITY.
FT  DISULFID      276     339     BY SIMILARITY.
FT  DISULFID      305     370     BY SIMILARITY.
FT  DISULFID      309     372     BY SIMILARITY.
FT  DISULFID      338     338     INTERCHAIN (BY SIMILARITY).
FT  CARBOHYD      54      54      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD     109     109     N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD     153     153     N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  SITE          224     226     CELL ATTACHMENT SITE (POTENTIAL).
SQ  SEQUENCE      373 AA;  42634 MW;  9903F3479C8552E5 CRC64;

```

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Query Match          49.2%;  Score 1067;  DB 1;  Length 373;
Best Local Similarity 53.5%;  Pred. No. 4e-78;
Matches 209;  Conservative 52;  Mismatches 98;  Indels 32;  Gaps 8;

```

```

Qy      30 LSTCKTIDMELVKRKRIEAIHQILSKLRLASPPSQGDVPPGPLPEAVLALYNSTRDRVA 89
      |||:| :|:| | :|:||||:|:|:|:|:|:|:|:| :| :| | |:| | | | |:| :
Db      2 LSTCQRLDLEAAKKKRIEAVRGQILSKLRLTAPPPASETPPRPLPDDVRALYNSTQELLK 61

Qy      90 GES-VEPEPEPEADYYAKEVTRVLMVESGNQIYDKFKGTPHSLYMLFNTSELREAVPEPV 148
      : : | |:| :|:|:|:| :| : : : : :|:|:|:| | | | |
Db      62 QRARLRPPPDGPDEYWAKELRRIPMETTWGAMEHWQPQSHSIFVFNVSRARRG-GRPT 120

```

```

QY      149 LLSRAELRLLRLKLK-----VEQHVELYQKYSNDSWRYLSNRLLAPSDSPEWLSFDVTGV 203
      || |||||:| | || :||| | | |||| | : : |||||
Db      121 LLHRAELRMLRQKAAADSAGTEQRLLEYQGYGNASWRYLHGRSVRATADDEWLSFDVTD 180

QY      204 VRQWLTRREAIEGFRLSAHCSCD---SKDNTLHVEINGFNSGRRGDLATIHGMNR--PFL 258
      | |||: | : |:|| | | : : | | :|||: | : | |::
Db      181 VHQWLSGSELLGVFKLSVHCPCMGPGHAEEMRISIEGFQ-QRGDMQSIKKHRRVPYV 239

QY      259 LLMATPLERAQHLHSSRRRALDNTNSYPYDVPDYASLALDNTNYCF--SSTEKNCCVRQLY 316
      | || | || | |||:| || |||:||| : ||||| ||
Db      240 LAMALPAERANELHSARRRR-----DLDTDYCFGPGTDEKNCCVRPLY 282

QY      317 IDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPASAAPCCVPQ 376
      ||||| ||||| |||||:||||| ||||:||||| ||||| |||||
Db      283 IDFRKDLQWKWIHEPKGYMANFCMGPCPYIWSADTQYTKVLALYNQHNPASAAPCCVPQ 342

QY      377 ALEPLPIVYVGRKPKVEQLSNMIVRSCKCS 407
      |:||||:||||| :|||||:|:||||
Db      343 TLDPLPIIYVGRNVRVEQLSNMVVRACKCS 373

```

RESULT 12

TGF1_XENLA

ID TGF1_XENLA STANDARD; PRT; 382 AA.

AC P16176;

DT 01-APR-1990 (Rel. 14, Created)

DT 01-APR-1990 (Rel. 14, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Transforming growth factor beta 1 precursor (TGF-beta 1) (TGF-beta 5).

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;

OC Xenopodinae; Xenopus.

OX NCBI_TaxID=8355;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=90110090; PubMed=2295601;

RA Kondaiah P., Sands M.J., Smith J.M., Fields A., Roberts A.B.,

RA Sporn M.B., Melton D.A.;

RT "Identification of a novel transforming growth factor-beta (TGF-beta

5) mRNA in Xenopus laevis.";

RL J. Biol. Chem. 265:1089-1093(1990).

RN [2]

RP SEQUENCE FROM N.A.

RA Vempati U.D., Kondaiah P.;

RL Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.

CC -!- FUNCTION: IMPORTANT ROLE IN CERTAIN ASPECTS OF DIFFERENTIATION.

CC -!- SUBUNIT: Homodimer; disulfide-linked.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the TGF-beta family.

CC -----
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DR EMBL; J05180; AAA49968.1; -.
DR EMBL; AF009335; AAB64441.1; -.
DR EMBL; AF009331; AAB64441.1; JOINED.
DR EMBL; AF009332; AAB64441.1; JOINED.
DR EMBL; AF009333; AAB64441.1; JOINED.
DR EMBL; AF009334; AAB64441.1; JOINED.
DR PIR; A34929; B61036.
DR HSSP; P01137; 1KLA.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR003911; TGF_TGFB.
DR InterPro; IPR001839; TGFB.
DR InterPro; IPR001111; TGFB_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFB_propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRINTS; PR01423; TGFBETA.
DR ProDom; PD000357; TGFB; 1.
DR SMART; SM00204; TGFB; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor; Mitogen; Glycoprotein; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT PROPEP 22 270
FT CHAIN 271 382 TRANSFORMING GROWTH FACTOR BETA 1.
FT DISULFID 277 286 BY SIMILARITY.
FT DISULFID 285 348 BY SIMILARITY.
FT DISULFID 314 379 BY SIMILARITY.
FT DISULFID 318 381 BY SIMILARITY.
FT DISULFID 347 347 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 123 123 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SITE 234 236 CELL ATTACHMENT SITE (POTENTIAL).
SQ SEQUENCE 382 AA; 44200 MW; 1034621C917AAE15 CRC64;

Query Match 40.9%; Score 887.5; DB 1; Length 382;
Best Local Similarity 46.4%; Pred. No. 1e-63;
Matches 192; Conservative 54; Mismatches 121; Indels 47; Gaps 11;

Qy 9 LPLLLPLLWLLVLTGPRPAAGLSTCKTIDMELVKRKRIEAIHQILSKLRLASPPSQGDV 68
: :| || |||| | |||| :||| |::| ||||| ||||| :| |
Db 1 MEVLWMLLVLLVHLSSLSLSTCKAVDMEEVRKRRIEAIHQILSKLKLDKTPDV-DS 59

Qy 69 PPGPLPEAVLALYNSTRDRVAGESVEPE----PEPEADYYAKEVTRVLMVESGNQIYDK 123
:| : ||||| : : : : | : ||||| :| | :| :|
Db 60 EKMTVPSEAIFLYNSTLEVIREKATREEEHVGHQNIQDYAKQVYR---FESITELED- 115

Qy 124 FKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKL--KVEQHVELYQKYSNDSW-- 179
| || :|| | || |||| : : : :| :|| :| :
Db 116 -----HEFKFKFNASHVRENVGMNSLLHHAELRMYKKQTDKNMDQRMELFWKYQENGTH 170

Qy 180 -RYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHCSC---DSKNTLHVE 235
||| : : | ||:|||| | :|| | | | | | :|| : :
Db 171 SRYLESKYITPVTDDWMSFDVTKTVNEWLKRAEENEQFGLQPACKCPTQAKD----ID 226

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QY      236  INGFNSGRRGDLATIHGM--NRPFLLLMATPLERAQHLHSSRHRRALDTNSYPYDVPDYA 293
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      227  IEGF-PALRGDLASLSSKENTKPYLMITSMIPAERIDTVTSSRKKR----- 270

QY      294  SLALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQY 353
      :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      271  --GVGQEYCFGNNGPNCCKVPLYINFRKDLGWKWIHEPKGYEANYCLGNCPYIWSMDTQY 328

QY      354  SKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      329  SKVLSLYNQNNPGASISPCCVPDVLEPLPIIYYVGRTAKVEQLSNMVVRSCNCS 382

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RESULT 13

TGF3_CHICK

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ID      TGF3_CHICK      STANDARD;      PRT;      412 AA.
AC      P16047;
DT      01-APR-1990 (Rel. 14, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Transforming growth factor beta 3 precursor (TGF-beta 3).
GN      TGFB3.
OS      Gallus gallus (Chicken).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC      Gallus.
OX      NCBI_TaxID=9031;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=89096966; PubMed=3211158;
RA      Jakowlew S.B., Dillard P.J., Kondaiiah P., Sporn M.B., Roberts A.B.;
RT      "Complementary deoxyribonucleic acid cloning of a novel transforming
RT      growth factor-beta messenger ribonucleic acid from chick embryo
RT      chondrocytes.";
RL      Mol. Endocrinol. 2:747-755(1988).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=White leghorn;
RX      MEDLINE=95169270; PubMed=7865129;
RA      Burt D.W., Dey B.R., Paton I.R., Morrice D.R., Law A.S.;
RT      "The chicken transforming growth factor-beta 3 gene: genomic
RT      structure, transcriptional analysis, and chromosomal location.";
RL      DNA Cell Biol. 14:111-123(1995).
RN      [3]
RP      SEQUENCE OF 1-117 FROM N.A.
RC      STRAIN=White leghorn; TISSUE=Blood;
RX      MEDLINE=92134496; PubMed=1840616;
RA      Burt D.W., Dey B.R., Paton I.R.;
RT      "Comparative analysis of human and chicken transforming growth
RT      factor-beta 2 and -beta 3 promoters.";
RL      J. Mol. Endocrinol. 7:175-183(1991).
RN      [4]
RP      SEQUENCE OF 1-117 FROM N.A.
RX      MEDLINE=93024487; PubMed=1406706;
RA      Jakowlew S.B., Lechleider R., Geiser A.G., Kim S.J.,
RA      Santa-Coloma T.A., Cubert J., Sporn M.B., Roberts A.B.;
RT      "Identification and characterization of the chicken transforming

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RT  growth factor-beta 3 promoter.";
RL  Mol. Endocrinol. 6:1285-1298(1992).
CC  -!- FUNCTION: INVOLVED IN EMBRYOGENESIS AND CELL DIFFERENTIATION.
CC  -!- SUBUNIT: Homodimer; disulfide-linked.
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- SIMILARITY: Belongs to the TGF-beta family.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; M31154; AAA49089.1; -.
DR  EMBL; X58127; CAA41128.2; -.
DR  EMBL; X60055; CAA41128.2; JOINED.
DR  EMBL; X60091; CAA41128.2; JOINED.
DR  EMBL; X60090; CAA41128.2; JOINED.
DR  EMBL; S46000; AAB23575.1; -.
DR  PIR; A34939; A34939.
DR  HSSP; P10600; 1TGJ.
DR  InterPro; IPR002400; GF_cysknot.
DR  InterPro; IPR003911; TGF_TGFB.
DR  InterPro; IPR001839; TGFB.
DR  InterPro; IPR001111; TGFB_N.
DR  Pfam; PF00019; TGF-beta; 1.
DR  Pfam; PF00688; TGFB_propeptide; 1.
DR  PRINTS; PR00438; GFCYSKNOT.
DR  PRINTS; PR01423; TGFBETA.
DR  ProDom; PD000357; TGFB; 1.
DR  SMART; SM00204; TGFB; 1.
DR  PROSITE; PS00250; TGF_BETA_1; 1.
KW  Growth factor; Mitogen; Glycoprotein; Signal.
FT  SIGNAL          1      23      POTENTIAL.
FT  PROPEP          24     300
FT  CHAIN           301     412      TRANSFORMING GROWTH FACTOR BETA 3.
FT  DISULFID        307     316      BY SIMILARITY.
FT  DISULFID        315     378      BY SIMILARITY.
FT  DISULFID        344     409      BY SIMILARITY.
FT  DISULFID        348     411      BY SIMILARITY.
FT  DISULFID        377     377      INTERCHAIN (BY SIMILARITY).
FT  CARBOHYD         74      74      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD        135     135      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD        142     142      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  SITE            261     263      CELL ATTACHMENT SITE (POTENTIAL).
FT  CONFLICT        323     326      ELPT -> DFRQ (IN REF. 1).
SQ  SEQUENCE       412 AA;  47077 MW;  1CAB883170069D55 CRC64;

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Query Match          40.1%;  Score 869.5;  DB 1;  Length 412;
Best Local Similarity 45.5%;  Pred. No. 3.1e-62;
Matches 195;  Conservative 56;  Mismatches 117;  Indels 61;  Gaps 13;

```

```

Qy      15 LLWLLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVPPGGLP 74
      |:|:|:  :  ||:| |:|:| :|:|:||||||| |||  | | :|
Db      9  LVLLSLLSFATVSLALSSCTTLDLEHIKKRVEAIRGQILSKLRLTSPPE--SVGPAHVP 66

```

Qy 75 EAVLALYNSTRDRVAGESVEPEPE-----PEADYYAKEVTRVLMVE---SGNQIYDKF 124
 :|||||: : | :| | | |::|||: : |: : |:
 Db 67 YQILALYNSTRELL--EEMEEEEKEESCSQENTESEYYAKEIHKFDMIQGLPEHNELGICP 124

Qy 125 KGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL---KLKVEQHVELYQKYSND--- 177
 || ::: || | | ||| |:|: : || :||:| |
 Db 125 KGVTSNVFR-FNVS---SAEKNSTNLFRAEFRVLRVPNPSSKRSEQRIELFQILRPDEHI 180

Qy 178 -SWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHCSC-----D 226
 |||| : ||||| ||:| | :| || | :
 Db 181 AKQRYLSGRNVQTRGSPEWLSFDVTDTVREWLLHRESNLGLEISIHCPCHTFQPNGDILE 240

Qy 227 SKDNTLHVEINGFNSG---RRGDLATI---HGMNRPFLLLMATPLERAQH--LHSSRHRR 278
 : | : : | : | : : | :| | | : | :|
 Db 241 NLHEVLEIKFKGIDSEDDYGRGDLGRLKKQKDLHNPHLILMMLPPHRLESPTLGGQRKKR 300

Qy 279 ALDTNSYPYDVPDYASLALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANF 338
 ||||| : |:| ||| : |||||: ||||| ||
 Db 301 -----ALDTNYCFRNLEENCCVRPLYIELPTDLGWKWVHEPKGYFANF 343

Qy 339 CLGPCPYIWSLDTQYSKVLALYNQHNPASAAAPCCVPQALEPLPIVYYVGRKPKVEQLSN 398
 | ||||: | || :| || || | |||: |||| | ||| :||| | |||||
 Db 344 CSGPCPYLRSADTTHSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSN 403

Qy 399 MIVRSCKCS 407
 |:|:|||||
 Db 404 MVVKSCCKCS 412

RESULT 14

TGF3_PIG

ID TGF3_PIG STANDARD; PRT; 409 AA.
 AC P15203;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Transforming growth factor beta 3 precursor (TGF-beta 3).
 GN TGFB3.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RX MEDLINE=89091120; PubMed=3208746;
 RA Derynck R., Lindquist B., Lee A., Wen D., Tamm J., Graycar J.L.,
 RA Rhee L., Mason A.J., Miller D.A., Coffey R.J., Moses H.L.,
 RA Chen E.Y.;
 RT "A new type of transforming growth factor-beta, TGF-beta 3."
 RL EMBO J. 7:3737-3743(1988).
 CC -!- FUNCTION: INVOLVED IN EMBRYOGENESIS AND CELL DIFFERENTIATION.
 CC -!- SUBUNIT: Homodimer; disulfide-linked.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the TGF-beta family.
 CC -----

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CC -----

DR EMBL; X14150; CAA32363.1; -.
DR PIR; S01825; S01825.
DR HSSP; P10600; 1TGJ.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR003911; TGF_TGFB.
DR InterPro; IPR001839; TGFB.
DR InterPro; IPR001111; TGFB_N.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFB_propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRINTS; PR01423; TGFBETA.
DR ProDom; PD000357; TGFB; 1.
DR SMART; SM00204; TGFB; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor; Mitogen; Glycoprotein; Signal.
FT SIGNAL 1 18 POTENTIAL.
FT PROPEP 19 297
FT CHAIN 298 409 TRANSFORMING GROWTH FACTOR BETA 3.
FT DISULFID 304 313 BY SIMILARITY.
FT DISULFID 312 375 BY SIMILARITY.
FT DISULFID 341 406 BY SIMILARITY.
FT DISULFID 345 408 BY SIMILARITY.
FT DISULFID 374 374 INTERCHAIN (BY SIMILARITY).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SITE 259 261 CELL ATTACHMENT SITE (POTENTIAL).
SQ SEQUENCE 409 AA; 46814 MW; B4900235B5CC955E CRC64;

Query Match 39.2%; Score 851; DB 1; Length 409;
Best Local Similarity 44.6%; Pred. No. 9.3e-61;
Matches 190; Conservative 58; Mismatches 122; Indels 56; Gaps 13;

Qy 15 LLWLLVLTTPGRPAAGLSTCKTIDMELVKRKRIEAIHQILSKLRLASPPSQGDVPPGPLP 74
|:|:| : :||| |:| : :|||:|||||:||||| : :|
Db 7 LVVLALLNFATVSLSMSTCTTLDHDKRKRVIAHQILSKLRLTSPDPMSML--ANIP 64

Qy 75 EAVLALYNSTR---DRVAGESVE--PEPEPEADYYAKEVTRVLMV---ESGNQIYDKFKG 126
|| ||||| : | || : : :|||:| : | : | : ||
Db 65 TQVLDLYNSTRELLEEVHGERGDDCTQENTESEYYAKEIYKFDMIQGLEEHNDLAVCPKG 124

Qy 127 TPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL---KLKVEQHVELYQKYSND---S 178
: : || | : : | ||| |:|: : || :||:| |
Db 125 ITSKIFR-FNVSSVEK---NETNLFRAEFRLRMPNPSSKRSEQRIELFQILQPDEHIAK 180

Qy 179 WRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHCSC-----DSK 228
||: : | : ||||| ||:| |||: | :| ||| : :
Db 181 QRYIDGKNLPTRGAAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNGDILENI 240

```

Qy      229 DNTLHVEINGFNS---GRRGDLATIHGM--NRPFLLLMATPLERAQH--LHSSRHRRALD 281
      :  ::  |  :|      ||||  :      :  |  :||  |  :|  :  |  :  |
Db      241 QEVM EIKFKGVDS EDDPGRGDLGRLKKKKEHSPHLILMMIPDRLDNPGGLGAQRKKR--- 297

Qy      282 TNSYPYDVPDYASLALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLG 341
      |||||  ||||  :  |  :|||  |||||  :|||  :|||  :|||  :|||  |
Db      298 -----ALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWWHEPKGYANFCSG 343

Qy      342 PCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYVGRKPKVEQLSNMIV 401
      |||  :  |  ||  :|  ||  ||  |||  :|||  |||  |  :|||  |||||  :|
Db      344 PCPYLRSADTTHSSVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTAKVEQLSNMVV 403

Qy      402 RSCKCS 407
      :|||
Db      404 KSCKCS 409

```

RESULT 15

TGF3_MOUSE

```

ID      TGF3_MOUSE      STANDARD;      PRT;      410 AA.
AC      P17125;
DT      01-AUG-1990 (Rel. 15, Created)
DT      01-AUG-1990 (Rel. 15, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Transforming growth factor beta 3 precursor (TGF-beta 3).
GN      TGFB3.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=90190650; PubMed=2628730;
RA      Miller D.A., Lee A., Matsui Y., Chen E.Y., Moses H.L., Derynck R.;
RT      "Complementary DNA cloning of the murine transforming growth
RT      factor-beta 3 (TGF beta 3) precursor and the comparative expression
RT      of TGF beta 3 and TGF beta 1 messenger RNA in murine embryos and
RT      adult tissues.";
RL      Mol. Endocrinol. 3:1926-1934(1989).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=91000714; PubMed=2206556;
RA      Denhez F., Lafyatis R., Kondaiah P., Roberts A.B., Sporn M.B.;
RT      "Cloning by polymerase chain reaction of a new mouse TGF-beta,
RT      mTGF-beta 3.";
RL      Growth Factors 3:139-146(1990).
CC      -!- FUNCTION: INVOLVED IN EMBRYOGENESIS AND CELL DIFFERENTIATION.
CC      -!- SUBUNIT: Homodimer; disulfide-linked.
CC      -!- SUBCELLULAR LOCATION: Secreted.
CC      -!- SIMILARITY: Belongs to the TGF-beta family.

```

```

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CC -----

DR EMBL; M32745; AAA40422.1; -.

DR PIR; A41397; A41397.

DR HSSP; P10600; 1TGJ.

DR MGD; MGI:98727; Tgfb3.

DR InterPro; IPR002400; GF_cysknot.

DR InterPro; IPR003911; TGF_TGFb.

DR InterPro; IPR001839; TGFb.

DR InterPro; IPR001111; TGFb_N.

DR Pfam; PF00019; TGF-beta; 1.

DR Pfam; PF00688; TGFb_propeptide; 1.

DR PRINTS; PR00438; GFCYSKNOT.

DR PRINTS; PR01423; TGFBETA.

DR ProDom; PD000357; TGFb; 1.

DR SMART; SM00204; TGFB; 1.

DR PROSITE; PS00250; TGF_BETA_1; 1.

KW Growth factor; Mitogen; Glycoprotein; Signal.

FT SIGNAL 1 23 POTENTIAL.

FT PROPEP 24 298 POTENTIAL.

FT CHAIN 299 410 TRANSFORMING GROWTH FACTOR BETA 3.

FT DISULFID 305 314 BY SIMILARITY.

FT DISULFID 313 376 BY SIMILARITY.

FT DISULFID 342 407 BY SIMILARITY.

FT DISULFID 346 409 BY SIMILARITY.

FT DISULFID 375 375 INTERCHAIN (BY SIMILARITY).

FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT SITE 259 261 CELL ATTACHMENT SITE (POTENTIAL).

SQ SEQUENCE 410 AA; 46884 MW; 250F7048CA432BD6 CRC64;

Query Match 38.9%; Score 844.5; DB 1; Length 410;
 Best Local Similarity 44.2%; Pred. No. 3.1e-60;
 Matches 188; Conservative 57; Mismatches 127; Indels 53; Gaps 12;

Qy 15 LLWLLVLTTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVPPGGLP 74
 |: |:| : |||| |:| :|:|:||||| ||| : :|
 Db 7 LVVLALLNLATISLSLSTCTTLDGHIKKRVEAIRGQILSKLRLTSPPEPSVMT--HVP 64

Qy 75 EAVLALYNSTR---DRVAGESVE--PEPEPEADYYAKEVTRVLMVE---SGNQIYDKFKG 126
 ||||| ||| : : || | : |::|||: : |:: |:: ||
 Db 65 YQVLALYNSTRELLEEMHGEREEGCTQETSESEYYAKEIHKFDMIQGLAEHNELAVCPKG 124

Qy 127 TPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL----KLKVEQHVELYQKYSND----S 178
 : : || | : : | || |:|: : | :|:| |
 Db 125 ITSKVFR-FNVSSVEK---NGTNLFRAEFRVLRVPNPSSKRTEQRIELFQILRPDEHIAK 180

Qy 179 WRYLSNRL LAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHCSC-----DSK 228
 ||: : | : ||||| ||:| ||: | :| || | :
 Db 181 QRYIGGKNLPTRGTAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNGDILENV 240

Qy 229 DNTLHVEINGFNS---GRRGDLATIHGM---NRPFLLMATPLERAQHLHSSRHRRALDT 282
 : : | : : |||| : : | |:| | | :
 Db 241 HEVMEIKFKGVDNEDDHGRGDLGRLKKQKDHHPHLLMMIPPHRLDSPGQGSQRK---- 296

Qy 283 NSYPYDVPDYASLALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGP 342

```

Db          297  -----KRALDTNYCFRNLEENCCVRPLYIDFRQDLGWKWVHEPKGYIANFCSGP 345
Qy          343  CPYIWSLDTQYSKVLALYNQHNP GASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVR 402
           |||: |||: |||| |||||: ||||| |||||: ||||| |||||: |||:
Db          346  CPYLR SADTTHSTVLGLYNTLNPEASASPCCVPQDLEPLTILYYVGRTPKVEQLSNMVVK 405
Qy          403  SCKCS 407
           |||||
Db          406  SCKCS 410

```

Search completed: October 28, 2003, 09:08:42
Job time : 9.15764 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

```
Run on:      October 28, 2003, 07:50:55 ; Search time 32.6306 Seconds
              (without alignments)
              3218.683 Million cell updates/sec
```

Title: US-10-017-372E-39
Perfect score: 2169
Sequence: 1 MAPSGRLRLPLLLPLLWLLV.....GRKPKVEQLSNMIVRSCKCS 407

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database : SPTREMBL 23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
```

```

14:  sp_unclassified:*
15:  sp_rvirus:*
16:  sp_bacteriap:*
17:  sp_archeap:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1835.5	84.6	390	6	Q9TUM8	Q9tum8 equus cabal
2	1756.5	81.0	368	11	Q8R4D9	Q8r4d9 sigmodon hi
3	868.5	40.0	379	13	Q8JHF5	Q8jhf5 sparus aura
4	864.5	39.9	379	13	Q8AXK8	Q8axk8 sparus aura
5	844.5	38.9	412	11	Q91YU7	Q91yu7 mus musculu
6	843	38.9	382	13	Q9PWA9	Q9pwa9 morone chry
7	841	38.8	414	11	Q91VP5	Q91vp5 mus musculu
8	826	38.1	382	13	O93449	O93449 oncorhynchu
9	787	36.3	376	13	Q9PTQ2	Q9ptq2 cyprinus ca
10	780	36.0	399	11	Q9ERB7	Q9erb7 mesocricetu
11	736.5	34.0	362	11	Q99K17	Q99k17 mus musculu
12	693.5	32.0	361	13	Q98854	Q98854 cyprinus ca
13	691.5	31.9	130	11	Q08714	Q08714 mesocricetu
14	674.5	31.1	124	6	Q95N80	Q95n80 canis famil
15	638	29.4	112	6	O02730	O02730 oryctolagus
16	620	28.6	255	11	Q921T1	Q921t1 mus musculu
17	604.5	27.9	127	6	Q9TV08	Q9tv08 canis famil
18	590	27.2	224	11	Q8CDZ9	Q8cdz9 mus musculu
19	580.5	26.8	200	13	Q90YF1	Q90yf1 pleuronecte
20	554	25.5	101	11	Q9R184	Q9r184 meriones un
21	476	21.9	179	13	Q90YF2	Q90yf2 pleuronecte
22	413	19.0	88	13	Q90YF5	Q90yf5 pleuronecte
23	402	18.5	88	13	Q90YF7	Q90yf7 oncorhynchu
24	397	18.3	88	13	Q90ZE7	Q90ze7 acipenser b
25	393	18.1	87	13	O42306	O42306 carassius a
26	388.5	17.9	309	4	Q8WV88	Q8wv88 homo sapien
27	383	17.7	91	6	Q9MYZ1	Q9myz1 capra hircu
28	373	17.2	86	6	Q28241	Q28241 cervus elap
29	358	16.5	81	6	Q9N1S3	Q9nls3 capreolus c
30	340	15.7	87	13	Q8JHB6	Q8jhb6 scophthalmu
31	336.5	15.5	375	13	Q8UWD8	Q8uwd8 columba liv
32	323.5	14.9	375	13	Q8AVB2	Q8avb2 coturnix co
33	321.5	14.8	375	13	Q8UWD7	Q8uwd7 coturnix ch
34	321.5	14.8	389	13	Q90YY0	Q90yy0 ictalurus p
35	317	14.6	77	13	Q90YF8	Q90yf8 oncorhynchu
36	316.5	14.6	375	13	Q98SP0	Q98sp0 gallus gall
37	313.5	14.5	375	6	Q9GM97	Q9gm97 equus cabal
38	313.5	14.5	375	13	Q8UWE0	Q8uwe0 anas platyr
39	311.5	14.4	375	13	Q8UWD9	Q8uwd9 anser anser
40	310.5	14.3	375	6	Q8HY52	Q8hy52 lepus capen
41	307.5	14.2	375	6	Q95J86	Q95j86 macaca fasc
42	302	13.9	50	6	Q28240	Q28240 cervus elap
43	301	13.9	62	13	Q90ZJ7	Q90zj7 anguilla an

44	300	13.8	62	13	Q90YF4	Q90yf4 pleuronecte
45	296.5	13.7	375	6	Q8WNS6	Q8wns6 bos taurus

ALIGNMENTS

RESULT 1

Q9TUM8

ID Q9TUM8 PRELIMINARY; PRT; 390 AA.
AC Q9TUM8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Transforming growth factor beta 1.
GN TGFBI.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RA Nixon A.J., Brower-Toland B.T., Sandell L.J.;
RT "Molecular cloning of equine transforming growth factor beta 1 reveals
RT a divergent nucleotide structure that encodes a novel bioactive
RT peptide among mammalian species.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF175709; AAD49431.1; -.
DR HSSP; P01137; 1KLA.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR InterPro; IPR003911; TGF_TGFb.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRINTS; PR01423; TGFbeta.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
SQ SEQUENCE 390 AA; 43860 MW; 220FE40DFCCA6016 CRC64;

Query Match 84.6%; Score 1835.5; DB 6; Length 390;
Best Local Similarity 86.0%; Pred. No. 2e-155;
Matches 350; Conservative 12; Mismatches 28; Indels 17; Gaps 1;

Qy	1	MAPSGLRLLPLLLPLLWLLVLT	TPGRPAAGLSTCKTIDMELVKRKRIE	AIRGQILSKLRLA	60
Db	1	MPPSGLRLLPLLLPLLWLLVLT	TPGRPAAGLSTCKTIDMELVKRKRIE	AIRGQILSKLRLA	60
Qy	61	SPPSQGDVPPGPLPEAVLALYNSTR	DRVAGESVEPEPEPEADYYAKEVTR	VLMMVESGNQI	120
Db	61	SPPSQGEVPPGPLPEAVLALYNSTR	AQVAGESAETEPEPEADYYAKEVTR	VLMMVEKENEI	120
Qy	121	YDKFKGTPHSLYMLFNTSELREAV	PEPVLLSRAELRLLRLKLKVEQHVELY	QKYSNDSWR	180

```

Db      121 YKTVETGSHSIYMFFNASELRRAAVPDPMLLSRAELRLLRLKLSVEQHVELYQKYSNNSWR 180
Qy      181 YLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHCSCDSKDNTLHVEINGFN 240
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      181 YLSNRLLTPSDSPEWLSFDVTGVVRQWLSQGGAMEGLRLSAHCPDCSKDNTLRVGINGFS 240
Qy      241 SGRRGDLATIHGMNRPFLLLMATPLERAQHLHSSRHRRALDTNSYPYDVPDYASLALDTN 300
        | ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      241 SSRRGDLATIDGMNRPFLLLMATPLERAQQLHSSRHRR-----ALDTN 283
Qy      301 YCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 360
        || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      284 YCSSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALY 343
Qy      361 NQHNPASAAAPCCVPQALEPLPIVYVGRKPKVEQLSNMIVRSCKCS 407
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      344 NQHNPASAAAPCCVPQVLEPLPIVYVGRKPKVEQLSNMIVRSCKCS 390

```

RESULT 2

Q8R4D9

```

ID   Q8R4D9          PRELIMINARY;          PRT;   368 AA.
AC   Q8R4D9;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Transforming growth factor beta-1 protein (Fragment).
GN   TGFb1.
OS   Sigmodon hispidus (Hispid cotton rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC   Sigmodon.
OX   NCBI_TaxID=42415;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Blanco J.C., Pletneva L.M., Prince G.A.;
RT   "Cotton rat cytokines, chemokines, and interferons.";
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR   EMBL; AF480858; AAL87199.1; -.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR001839; TGFb.
DR   InterPro; IPR001111; TGFb_N.
DR   Pfam; PF00019; TGF-beta; 1.
DR   Pfam; PF00688; TGFb_propeptide; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   ProDom; PD000357; TGFb; 1.
DR   SMART; SM00204; TGFb; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
FT   NON_TER      1          1
SQ   SEQUENCE      368 AA;  41905 MW;  A5C91207B0468B4A CRC64;

```

```

Query Match      81.0%;  Score 1756.5;  DB 11;  Length 368;
Best Local Similarity  84.9%;  Pred. No. 2.1e-148;
Matches 327;  Conservative 16;  Mismatches 25;  Indels 17;  Gaps 1;

```

```

Qy      23 PGRPAAGLSTCKTIDMELVKRKRIEAI RQILSKLRLASPPSQGDVPPGPLPEAVLALYN 82

```

```

      |||
Db      1 PGRPAAGLSTCKTIDMELVKKRIEAI RGQILSKLRLASPPSQGEVPPGPLPEAVLALYN 60
Qy      83 STRDRVAGESVEPEPEPEADYYAKEVTRVLMVESGNQIYDKFKGTPHSLYMLFNTSELRE 142
      |||
Db      61 STRDRVAGESADPEPEPEADYYAKEVTRVLMVDRNNAIYDKTKDIPHSVYMFNTSDIRE 120
Qy      143 AVPEPVLLSRAELRLLRLKLKVEQHVELYQKYSNDSWRYLSNRLLAPSDSPEWLSFDVTG 202
      |||
Db      121 AVPEPPLLSRAELRLQRFKSNVEQHVELYEKYSNNSWRYLGNRLLSPTDSPWLSFDVTS 180
Qy      203 VVRQWLTRREAIEGFRLSAHCSKCDSDNTLHVEINGFNSGRRGDLATIHGMNRPFLLLMA 262
      |||
Db      181 VVRKWLNQGDGIQGRFSAHCSKCDSDNILHVEINGISPKRRGDLGTIHDNRPFLLLMA 240
Qy      263 TPLERAQHLHSSRHRRALDTSYPYDVPDYASLALDTSNYCFSSTEKNCCVRQLYIDFRKD 322
      |||
Db      241 TPLERAQHLHSSRHR-----ALDTSNYCFSSTEKNCCVRQLYIDFRKD 283
Qy      323 LGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNP GASAAPCCVPQALEPLP 382
      |||
Db      284 LGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNP GASASPCCVPQALEPLP 343
Qy      383 IVYYVGRKPKVEQLSNMIVRSCKCS 407
      |||
Db      344 IVYYVGRKPKVEQLSNMIVRSCKCS 368

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RESULT 3

Q8JHF5

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ID      Q8JHF5          PRELIMINARY;          PRT;    379 AA.
AC      Q8JHF5;
DT      01-OCT-2002 (TrEMBLrel. 22, Created)
DT      01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT      01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE      Transforming growth factor beta 1.
OS      Sparus aurata (Gilthead sea bream).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC      Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
OC      Sparidae; Sparus.
OX      NCBI_TaxID=8175;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Tafalla C., Aranguren R., Secombes C.J., Castrillo J.L., Novoa B.,
RA      Figueras A.;
RT      "Molecular characterization of sea bream (Sparus aurata) transforming
RT      growth factor beta1.";
RL      Fish and Shellfish Immunol. 0:0-0(2002).
CC      -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR      EMBL; AF510084; AAN03842.1; -.
DR      InterPro; IPR002400; GF_cysknot.
DR      InterPro; IPR001839; TGFb.
DR      InterPro; IPR001111; TGFb_N.
DR      InterPro; IPR003911; TGF_TGFb.
DR      Pfam; PF00019; TGF-beta; 1.
DR      Pfam; PF00688; TGFb_propeptide; 2.

```


RT "Molecular cloning and characterization of sea bream (*Sparus aurata*)
RT TGF beta 1.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF424703; AAN76665.1; -.
SQ SEQUENCE 379 AA; 43485 MW; A306EC387F6DBA7C CRC64;

Query Match 39.9%; Score 864.5; DB 13; Length 379;
Best Local Similarity 46.2%; Pred. No. 1e-68;
Matches 189; Conservative 70; Mismatches 105; Indels 45; Gaps 16;

Qy 12 LLPLLWLLVLTTPGRPAAGLSTCKTIDMELVKRKRIEAIHQILSKLRL-ASPPSQGDVPP 70
|:|:::| |: :|:||||:|:|:|:||||| ||||| | ||
Db 3 LVFLMFMVAYTVGK-VSGMSTCKTLDLEMVKKKRIEAIHQILSKLRLPTESPQAGD--E 59

Qy 71 GPLPEAVLALYNSTRDRVAGESVEPEPE-----PEADYYAKEVTRVLMVESGNQIYDKFK 125
:| :|:|:||||: : : | : : | :|:| ||| :| :
Db 60 EEIPSSLLSLYNSTKEMLKEQQTEVQTDIFTEXEEYFA---TRVHKFNNTNPV----- 111

Qy 126 GTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLKV--EQHVELYQKYSNDSWRYL 182
|| :| | |||:| : : ||: ||||:| :| || |||| | |||
Db 112 RTPQNMSMSFNISEIRRSIGDYRLTTAELRML-IKAPTILDEQRVELYQGLGT-SPRYL 169

Qy 183 SNRLLAPSDSPEWLSFDVTVGVVRQWLTRREAIEGFRLSAHCSC--DSKDNTLHVEINGFN 240
::| : :|:||||| :| || : :| :| | :| :| :|
Db 170 ASRFITNELRDKWLSFDVTETLQNWLGKNDVQVFQLRLYCDCGRSSDVSTFSFGISGMT 229

Qy 241 SGRRGDLATIHGMNR--PFLLLMATPLERAQHLHSSRHRRALDTNSYPYDVPDYASLALD 298
:| ||| | : | :| :| :| :| :| :| :| :| :| :|
Db 230 AG-RGDKAVLDDMTKQPPYILTMSIPKNVSSHL-TSRKKRSTETK-----D 273

Qy 299 TNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVL 358
| | : || |||| ||||| |||||:| ||||:|:| | |||: : :||: ||
Db 274 T--CTAQTE-TCCVRSLYIDFRKDLGWKWIHKPTRYHANYCMGSCTYIWNENKYSQXLA 330

Qy 359 LYNQHNPASAAAPCCVPQALEPLPIVYVGRKPKVEQLSNMIVRSCKCS 407
|| ||||| ||||| |||||:||||: ||||| |||||:|||||
Db 331 LYKHHNPASAAAPCCVPQALEPLPIVYVGRQHKVEQLSNMIVKSKCS 379

RESULT 5

Q91YU7

ID Q91YU7 PRELIMINARY; PRT; 412 AA.
AC Q91YU7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Transforming growth factor, beta 3.
GN TGFB3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

DR EMBL; BC014690; AAH14690.1; -.
DR MGD; MGI:98727; Tgfb3.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR001839; TGFb.
DR InterPro; IPR001111; TGFb_N.
DR InterPro; IPR003911; TGF_TGFb.
DR Pfam; PF00019; TGF-beta; 1.
DR Pfam; PF00688; TGFb_propeptide; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR PRINTS; PR01423; TGFbBETA.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFb; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
SQ SEQUENCE 412 AA; 47144 MW; F3EB65D046DF32AD CRC64;

Qy	15	LLWLLVLTGPRPAAGLSTCKTIDMELVKRKRIEAI	RGQILSKLRLASPPSQGDVPPGPLP	74
Db	9	LVLALLNLATISLSLSTCTTLD	FGHIKKRVEAIRGQILSKLRLTSPPEPSVMT--HVP	66
Qy	75	EAVLALYNSTR---	DRVAGESVE--PEPEPEADYYAKEVTRVLMVE---SGNQIYDKFKG	126
Db	67	YQVLALYNSTRELLEEMHGEREEGCTQETSESEYYAKEIHKFD	MIQGLAEHNELAVCPKG	126
Qy	127	TPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL----	KLKVEQHVELYQKYSND----S	178
Db	127	ITSKVFR-FNVSSVEK---	NGTNLFRAEFVRLRVPNPSSKRTEQRIELFQILRPDEHIAK	182
Qy	179	WRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHCSC-----	DSK	228
Db	183	QRYIGGKNLPTRGTAEWLSFDVTDTVREWLLRRESNLGLEISIHCPCHTFQPNGDILENV		242
Qy	229	DNTLHVEINGFNS--	GRRGDLATI HGM---NRPFLLLMATPLERAQHLHSSRHRRALDT	282
Db	243	HEVMEIKFKGVDNEDDHGRGDLGRLKKQKDHHNPHLI	LMMIPPHRLDSPGQGSQRK----	298
Qy	283	NSYPYDVPDYASLALDNTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGP		342
Db	299	-----	KRALDNTNYCFRNLEENCCVRPLYIDFRQDLGWKVWHEPKGYANFCSGP	347
Qy	343	CPYIWSLDTQYSKVLALYNQHNP	GASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVR	402
Db	348	CPYLRSADTTHSTVLGLYNTLNPEASASPCCVQDLEPLTILYYVGRTPKVEQLSNMIVK		407
Qy	403	SCKCS	407	
Db	408	SCKCS	412	

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Transforming growth factor beta precursor.
 GN TGF-BETA.
 OS Morone chrysops x Morone saxatilis (white bass x striped bass).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidei;
 OC Moronidae; Morone.
 OX NCBI_TaxID=45352;
 RN [1]
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RC TISSUE=KIDNEY;
 RX MEDLINE=20394636; PubMed=10938723;
 RA Harms C.A., Kennedy-Stoskopf S., Horne W.A., Fuller F.J.,
 RA Tompkins W.A.F.;
 RT "Cloning and sequencing hybrid striped bass (Morone saxatilis x M.
 RT chrysops) transforming growth factor-beta (TGF-beta), and development
 RT of a reverse transcription quantitative competitive polymerase chain
 RT reaction (RT-qcPCR) assay to measure TGF-beta mRNA of teleost fish."
 RL Fish Shellfish Immunol. 10:61-85(2000).
 CC -!- FUNCTION: IS LIKELY TO BE AN IMPORTANT CYTOKINE REGULATING IMMUNE
 CC RESPONSE. MAY ALSO HAVE A ROLE IN OTHER PHYSIOLOGICAL SYSTEMS.
 CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
 CC -!- TISSUE SPECIFICITY: HIGHER LEVELS FOUND IN MONONUCLEAR CELLS FROM
 CC PERIPHERAL BLOOD THAN IN SPLEEN OR ANTERIOR KIDNEY.
 CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 DR EMBL; AF140363; AAD46997.1; -.
 DR HSSP; P01137; 1KLA.
 DR InterPro; IPR002400; GF_cysknot.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb_N.
 DR InterPro; IPR003911; TGF_TGFb.
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR PRINTS; PR00438; GFCYSKNOT.
 DR PRINTS; PR01423; TGFBETA.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFB; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Growth factor; Mitogen; Glycoprotein; Signal.
 FT SIGNAL 1 ? POTENTIAL.
 FT PROPEP ? 270
 FT CHAIN 271 382 TRANSFORMING GROWTH FACTOR BETA.
 FT DISULFID 278 286 BY SIMILARITY.
 FT DISULFID 285 348 BY SIMILARITY.
 FT DISULFID 314 379 BY SIMILARITY.
 FT DISULFID 318 381 BY SIMILARITY.
 FT DISULFID 347 347 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 73 73 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 108 108 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 124 124 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SITE 235 237 CELL ATTACHMENT SITE (POTENTIAL).
 SQ SEQUENCE 382 AA; 43846 MW; 3124D8C34EA74D72 CRC64;

Query Match 38.9%; Score 843; DB 13; Length 382;
 Best Local Similarity 45.0%; Pred. No. 8.5e-67;
 Matches 185; Conservative 67; Mismatches 107; Indels 52; Gaps 14;

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Qy      15 LLWLLVLTTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRL--ASPPSQGDVPPG 71
      | : : : | | : : | | | | : : | : | | | | | | | | | | | | | |
Db      6 LMLVVVYTVGN-VSGMSTCKTLDLEMVKKKRIEAI RSQILSKLRLPKPEPEPDQAGDEEEI 64

Qy     127 PLPEAVLALYNSTRDRVAGESVEPE-----PEPEADYYAKEVTRVLMVESGNQIYDKFKG 126
      | | : : | | | | : : : | : : : | : : | | : : | |
Db     65 PTP--LLSLYNSTKEMLKEQQTEVQTDISTEQEEEEYFAKVLHKFNMTRKNN----- 114

Qy     127 TPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLV--EQHVELYQKYSNDSWRYLSN 184
      | : | | | | : : | : | | : | | : | | | | | | | | | | : :
Db    115 TDTTKKMFFNISEIRESVGDYRLLTSAELRMLIKKTTIYDEQRVELYSGL-GDSPRYLAS 173

Qy     185 RLLAPSDSPEWLSFDVTGVVRQWLTRREAI EGFRLSAHCSCD---SKDNTLHVEINGFNS 241
      | : : : | | | | : : | | : : | : | | | | : : : | : :
Db    174 RFITNKWKDKWLSFDVTKTLDQWLKGTDDQGFQLRLFCENKVSAGETIFKFGISGIDP 233

Qy     242 GRRGDLATIHGMNR--PFLLLMATPLERAQHLHS---SRHRRALDTSYPYDVPDYASLA 296
      | | | | : : : | : | | : | | : | | : | : | : |
Db    234 G-RGDTGPMQLLTQQPPYILTMSIP---QNISSPSTSRKKRSTETK----- 275

Qy     297 LDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKV 356
      : | : | | | | | | | | | | | | | | : | : | : | | | : : :
Db    276 ---DVCTAQTE-TCCVRSLYIDFRKDLGWKWIHKPTGYNANYCMGSCTYIWNENKYSQI 331

Qy     357 LALYNQHNP GASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
      | | | | | | | | | | | | | | : | | | : | | | | | | : | | |
Db    332 LALYKHHNPGASAPCCVPQALEPLPIVYYVGRQHKEQLSNMIVKSKCS 382
  
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RESULT 7

Q91VP5

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ID   Q91VP5          PRELIMINARY;          PRT;    414 AA.
AC   Q91VP5;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Similar to transforming growth factor, beta 2.
GN   TGFB2.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Breast tumor;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR   EMBL; BC011170; AAH11170.1; -.
DR   MGD; MGI:98726; Tgfb2.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR001839; TGFb.
DR   InterPro; IPR001111; TGFb_N.
  
```

DR InterPro; IPR003911; TGF_TGFb.
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR PRINTS; PR00438; GFCYSKNOT.
 DR PRINTS; PR01423; TGFBETA.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFB; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 SQ SEQUENCE 414 AA; 47588 MW; DB37A7C38881F286 CRC64;

Query Match 38.8%; Score 841; DB 11; Length 414;
 Best Local Similarity 43.8%; Pred. No. 1.4e-66;
 Matches 190; Conservative 62; Mismatches 120; Indels 62; Gaps 15;

Qy	12	LLPLLWLLVLTTPGRPAAGLSTCKTIDMELVKRKRIE	AIRGQILSKLRLASPPSQGDVP-P	70
		: : : :		
Db	5	VLSTFLLHLVLP--VALSLSTCSTLDMQFMRKRIE	AIRGQILSKLKLTSPP--DYPEP	60
Qy	71	GPLPEAVLALYNSTRD---RVAGESVEPEPE-PEADYYAKEVTRVLM---	VESGNQIYD	122
		: :: : : : : : : : :		
Db	61	DEVPPEVISIYNSTRDLLQEKASRRAAACERERSDEEYYAKEVYKIDMP	SHLPSENAIPP	120
Qy	123	KFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL---	KLKV-EQHVELYQ-----K	173
		: : : : : : :		
Db	121	TFY-RPYFRIVRFDVSTMEKNASN--LVKAEFRVFRQLQNP	KARVAEQRIELYQILKSKD	176
Qy	174	YSNDSWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHCSC-----		225
		: : : : : : : : :		
Db	177	LTSPTQRYIDSKVVKTRAEGEWLSFDVTDVQEWLHHKDRNLGFKISLHCP	CCTFVPSNN	236
Qy	226	---DSKDNTLHVE---INGFNSGRRGDLATIHGMR-----PFLLLMATPLERAQHLHS		273
		: : : : : :		
Db	237	YIIPNKSEELEARFAGIDGTSTYASGDQKTIKSTRKKTSGKTPHLLLMLLPSYRLESQQS		296
Qy	274	SRHRRALDTNSYPYDVPDYASLALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKG		333
		: : : : : :		
Db	297	SRRKKR-----ALDAAYCFRNVQDNCCLRPLYIDFKRDLGWKWIHEPKG		340
Qy	334	YHANFCLGPCPYIWSLDTQYSKVLALYNQHNP	GASAAPCCVPQALEPLPIVYYVGRKPKV	393
		: : : : : : :		
Db	341	YNANFCAGACPYLWSSDTQHTKVLSLYNTINPEASASPCCVSDLEPLTILYYIGNTPKI		400
Qy	394	EQLSNMIVRSCKCS		407
		:		
Db	401	EQLSNMIVKSCCKCS		414

RESULT 8
 O93449
 ID O93449 PRELIMINARY; PRT; 382 AA.
 AC O93449; Q91217;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Transforming growth factor beta precursor.
 GN TGF-BETA OR TGF.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LEUKOCYTE;
 RX MEDLINE=99242020; PubMed=10227481;
 RA Daniels G.D., Secombes C.J.;
 RT "Genomic organisation of rainbow trout, *Oncorhynchus mykiss* TGF-
 RT BETA.";
 RL Dev. Comp. Immunol. 23:139-147(1999).
 RN [2]
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
 RC TISSUE=LEUKOCYTE;
 RX MEDLINE=98390168; PubMed=9722928;
 RA Hardie L.J., Laing K.J., Daniels G.D., Grabowski P.S., Cunningham C.,
 RA Secombes C.J.;
 RT "Isolation of the first piscine transforming growth factor beta gene:
 RT analysis reveals tissue specific expression and a potential regulatory
 RT sequence in rainbow trout (*Oncorhynchus mykiss*).";
 RL Cytokine 10:555-563(1998).
 CC -!- FUNCTION: IS LIKELY TO BE AN IMPORTANT CYTOKINE REGULATING IMMUNE
 CC RESPONSE. MAY ALSO HAVE A ROLE IN OTHER PHYSIOLOGICAL SYSTEMS.
 CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN BLOOD LEUKOCYTES, KIDNEY
 CC MACROPHAGES, BRAIN, GILL AND SPLEEN BUT NOT IN LIVER.
 CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 DR EMBL; AJ007836; CAA07707.1; -.
 DR EMBL; X99303; CAA67685.1; -.
 DR HSSP; P01137; 1KLA.
 DR InterPro; IPR002400; GF_cysknot.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb_N.
 DR InterPro; IPR003911; TGF_TGFb.
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR PRINTS; PR00438; GFCYSKNOT.
 DR PRINTS; PR01423; TGFbBETA.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Growth factor; Mitogen; Glycoprotein; Signal.
 FT SIGNAL 1 20 POTENTIAL.
 FT PROPEP 21 270
 FT CHAIN 271 382 TRANSFORMING GROWTH FACTOR BETA.
 FT DISULFID 278 286 BY SIMILARITY.
 FT DISULFID 285 348 BY SIMILARITY.
 FT DISULFID 314 379 BY SIMILARITY.
 FT DISULFID 318 381 BY SIMILARITY.
 FT DISULFID 347 347 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 76 76 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 116 116 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 125 125 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 237 237 N -> D (IN REF. 2).
 FT CONFLICT 345 345 Q -> H (IN REF. 2).
 FT CONFLICT 371 372 LS -> VP (IN REF. 2).

Query Match 38.1%; Score 826; DB 13; Length 382;
Best Local Similarity 46.8%; Pred. No. 2.8e-65;
Matches 184; Conservative 57; Mismatches 104; Indels 48; Gaps 14;

Qy	30	LSTCKTIDMELVVKRKRIEAIRGQILSKLRLASPP--SQGDVPPGGLPEAVLALYNSTRD	86
Db	23	MSTCKSLDLELVKKRKRIEAIRGQILSKLRLPKEPEIDQEGDTE--EVPASLMSIYNSTVE	80
Qy	87	RVAGESVE-----PEPEPEADYYAKEVTRVLMVESGNQIYDKFKGTPHSLYMLFNTSEL	140
Db	81	-LSEEQVHTYIPSTQDAEEEA-YFAKEVHKFNMQSENT-----SKHQI--LFNMSEM	129
Qy	141	REAVPEPVLLSRAELRLL---RLKLKVEQHVELYQKYSNDSWRYLSNRLLAPSDSPEWL	196
Db	130	RSVLGTDRLLSQAELRLLIKNHGLLDDSEQRLELYRGV-GDKARYLKSHFVSKEWANRWV	188
Qy	197	SFDVTGVVRQWLTRREAIEGFRLSAHCSCDSKDNTLHVEINGFNSGRRGDLATI--HGMN	254
Db	189	SFDVTQTLNEWLQGAGEEQGFQLKLPCDCGKPMEEFRFKISGMNK-LRGNTETLAMKMPS	247
Qy	255	RPFLLLMTPLERAQHLHSSRRHRRALDTSNYPYDVPDYASLALDNTNYCFSSTEKNCCVRQ	314
Db	248	KPHILLMSLPVERHSQL-SSRKKRQTTE-----EIC-SDKSESCCVRK	289
Qy	315	LYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPASAAAPCCV	374
Db	290	LYIDFRKDLGWKWIHEPTGYFANYCIGPCTYIWNTENKYSQVLALYKHHNPGASAPCCV	349
Qy	375	PQALEPLPIVYYYVGRKPKVEQLSNMIVRSCKCS	407
Db	350	PQVLEPLPIIYYVGRQHKVEQLSNMIVKSCRCS	382

Q9PTQ2

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ID      Q9PTQ2                PRELIMINARY;          PRT;    376 AA.
AC      Q9PTQ2;
DT      01-MAY-2000 (TrEMBLrel. 13, Created)
DT      01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT      01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE      Transforming growth factor beta precursor.
OS      Cyprinus carpio (Common carp).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC      Cyprinidae; Cyprinus.
UX      NCBI_TaxID=7962;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Yin Z., Kuang J.;
RT      "Molecular cloning of carp transforming growth factor beta 1.";
RL      Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
CC      -!- FUNCTION: IS LIKELY TO BE AN IMPORTANT CYTOKINE REGULATING IMMUNE
CC      RESPONSE. MAY ALSO HAVE A ROLE IN OTHER PHYSIOLOGICAL SYSTEMS.
CC      -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).

```

CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 DR EMBL; AF136947; AAF22573.1; -.
 DR HSSP; P01137; 1KLA.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb_N.
 DR InterPro; IPR003911; TGF_TGFb.
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR PRINTS; PR01423; TGFbeta.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFb; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Growth factor; Mitogen; Glycoprotein; Signal.
 FT SIGNAL 1 22 POTENTIAL.
 FT PROPEP 23 264
 FT CHAIN 265 376 TRANSFORMING GROWTH FACTOR BETA.
 FT DISULFID 272 280 BY SIMILARITY.
 FT DISULFID 308 373 BY SIMILARITY.
 FT DISULFID 312 375 BY SIMILARITY.
 FT DISULFID 341 341 INTERCHAIN (BY SIMILARITY).
 FT CARBOHYD 76 76 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 125 125 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 167 167 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT SITE 230 232 CELL ATTACHMENT SITE (POTENTIAL).
 SQ SEQUENCE 376 AA; 43329 MW; 7F7FC4DA58B69681 CRC64;

Query Match 36.3%; Score 787; DB 13; Length 376;
 Best Local Similarity 43.8%; Pred. No. 8.4e-62;
 Matches 180; Conservative 64; Mismatches 121; Indels 46; Gaps 15;

Qy 6 LRLPLLLPLWLLVLTGPRPAAGLSTCKTIDMELVKRKRIEAIHQILSKRLASPPSQ 65
 :|: ||| | || : |||| :|:|:| ||||| ||||| ||||| : |
 Db 1 MRVESLLLALQCLLGFV--HYSALSTCSPLDLELIKRIEAIHQILSKRLSKEPEV 58

Qy 66 GDVPPGP-LPEAVLALYNST---RDRVAGESVEPEPEP-EADYYAKEVTR--VLMVESGN 118
 : :| :||| : | :|:| | :||| : : :|
 Db 59 DEEKESQNI PAELISVYNSTVELNEEQAAPPEQPKEDPVEEYYAKEVHKFTIKLMEKNP 118

Qy 119 QIYDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRLKLGK--VEQHVELYQKYSN 176
 ||| : || :| : : :|:| ||| || :||| |
 Db 119 ---DKF-----LWFNITDISQTLGLNRIISQVELRLLITTFPDGSEQRLELYQVIGN 167

Qy 177 DSWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHCSCDSKDNTLHVEI 236
 | ||| :| : :| ||||| :| || | || :||| :|| : | :|
 Db 168 KS-RYLESRFI--PNQRKWLSDFTQTLKDWLQRSEAEQGFQLKMADNCDPQ-KTFQLKI 223

Qy 237 NGFNSGRRGDLATIH-GMNRPFLLLMATPLERAQHLHSSRRHRRALDTNSYPYDVPDYASL 295
 | ||| | : | || :|:| :| : : || :| :| :| :|
 Db 224 PGLVL-VRGDTETLAVNMPPHILVMSLPLD-GNNSKSRKRQTETDQVCTDKSD---- 277

Qy 296 ALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSK 355
 |||| ||||| ||||| ||||| ||||| :| :| :| :| :| :| :| :|
 Db 278 -----GCCVRSLYIDFRKDLGWKWIHEPSGYANYCTGSCSFVWTSENKYSQ 324

Qy 356 VLALYNQHNPASAAAPCCVPQALEPLPIVYVGRKPKVEQLSNMIVRSCKC 406
 ||||| ||||| || ||| ||||| ||||| : ||||| ||||| :|||
 Db 325 VLALYKHHPGASAPCRVPQVLNPLPIFYVGRQHKVEQLSNMIVKTCKC 375

RESULT 10

Q9ERB7

ID Q9ERB7 PRELIMINARY; PRT; 399 AA.
 AC Q9ERB7;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Transforming growth factor-beta 2 (Fragment).
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 OX NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ramesh G., Kondaiah P., Seshagiri P.B.;
 RT "Differential expression and selective localization of transforming
 RT growth factor-beta isoforms in the hamster uterus during estrous
 RT cycle.";
 RL Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
 CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 DR EMBL; AY007214; AAG02247.1; -.
 DR HSSP; P08112; 2TGI.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb_N.
 DR InterPro; IPR003911; TGF_TGFb.
 DR Pfam; PF00019; TGF-beta; 1.
 DR Pfam; PF00688; TGFb_propeptide; 1.
 DR PRINTS; PR01423; TGFBETA.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFB; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 FT NON_TER 1 1
 FT NON_TER 399 399
 SQ SEQUENCE 399 AA; 46078 MW; A6FF8E65EAFD5148 CRC64;

Query Match 36.0%; Score 780; DB 11; Length 399;
 Best Local Similarity 42.6%; Pred. No. 3.8e-61;
 Matches 179; Conservative 58; Mismatches 121; Indels 62; Gaps 15;

Qy 18 LLVLTPGRPAAGLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGDVP-PGPLPEA 76
 ||| | | |||| |:|:| | ||||| |||||:| ||| | | :|
 Db 4 LLHLVP--VALSLSTCSTLDMQFMRKRIEAIRGQILSKLKLTSPP--DYPEPDEVPE 59
 Qy 77 VLALYNSTRD----RVAGESVEPEPE-PEADYYAKEVTRVLM--VESGNQIYDKFKGTP 128
 |::| ||||| : : : | | : : ||||| : : | | | | | |
 Db 60 VISIYNSTRDLLQEKASRRAAACERERSDEEYYAKEVYKIDMPSHFPSENAIPPTFY-RP 118
 Qy 129 HSLYMLFNTSELREAVPEPVLLSRAELRLLRL---KLKV-EQHVELYQ-----KYSNDSW 179
 : : | : : | : || | | : | | : |||| : : :
 Db 119 YFRIVRFDVSMMEKNASN---LVKAEFRVRLQNPKEARVAEQRIELYQILKSKDLTSPTQ 175
 Qy 180 RYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSAHCSC-----DSK 228
 ||: :::: ||||| | : || : : ||: | | | :|
 Db 176 RYIDSKVVKTRAEGEWLSFDVTDVHEWLHHKDRNLGFKISLHCPCTFVPFNNNIIPNK 235


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QY      229 DNTLHVE---INGFNSGRRGDLATIHGMNR-----PFLLLMATPLERAQHLHSSRRHRA 279
      |      | : | :      | ||      :      | |||| | | : | : | :
Db      236 SEELEARFAGIDGTSQHSSGHQETIKSTRKKNSGKTPHLLMLLPSYRLESQQSNRRKKR 295

QY      280 LDTNSYPYDVPDYASIALDNTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFC 339
      ||| ||| : : |||:| |||||:| ||||| |||||:| |||
Db      296 -----ALDAAYCFRNVQDNCCLRPLYIDFKRDLGWKWIHEPKGYNANFC 339

QY      340 LGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVYYVGRKPKVEQLSNM 399
      | |||:| |||:| |||:| || |||:| ||| ||| | : ||| ||| |||
Db      340 AGACPYLWSSDTQHTKVLSLYNTINPEASASPCCVSHDLEPLTILYYIGNTPKIEQLSNM 399

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RESULT 11

Q99K17

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ID   Q99K17      PRELIMINARY;          PRT;   362 AA.
AC   Q99K17;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   Similar to transforming growth factor, beta 3 (Fragment).
GN   TGFB3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR   EMBL; BC005513; AAH05513.1; -.
DR   HSSP; P10600; 1TGJ.
DR   MGD; MGI:98727; Tgfb3.
DR   InterPro; IPR002400; GF_cysknot.
DR   InterPro; IPR001839; TGFB.
DR   InterPro; IPR001111; TGFB_N.
DR   InterPro; IPR003911; TGF_TGFB.
DR   Pfam; PF00019; TGF-beta; 1.
DR   Pfam; PF00688; TGFB_propeptide; 1.
DR   PRINTS; PR00438; GFCYSKNOT.
DR   PRINTS; PR01423; TGFBETA.
DR   ProDom; PD000357; TGFB; 1.
DR   SMART; SM00204; TGFB; 1.
DR   PROSITE; PS00250; TGF_BETA_1; 1.
FT   NON_TER      1      1
SQ   SEQUENCE      362 AA;  41486 MW;  0808E46180FDAE70 CRC64;

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Query Match          34.0%;   Score 736.5;   DB 11;   Length 362;
Best Local Similarity 42.9%;   Pred. No. 2.6e-57;
Matches 164;   Conservative 51;   Mismatches 114;   Indels 53;   Gaps 12;

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QY      58 RLASPPSQGDVPPGPLPEAVLALYNSTR---DRVAGESVE--PEPEPEADYYAKEVTRVL 112
      | : |||      :      | ||||| ||| : : || | : | : ||||| : :
Db      2  RVGSPPEPSVMT--HVPYQVLALYNSTRELLLEEMHGEREEGCTQETSESEYYAKEIHKFD 59

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Qy 113 MVE---SGNQIYDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL---KLKVE 165
 |:: |:: || :: || |:: | || |:: |:: : |
 Db 60 MIQGLAEHNELAVCPKGITSKVFR-FNVSSVEK---NGTNLFRAEFRVLVVPNPSSKRTE 115

Qy 166 QHVELYQKYSND----SWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRREAIEGFRLSA 221
 |::|::| |:: : | : ||||| |::| |:: | : |
 Db 116 QRIELFQILRPDEHIAKQRYIGGKNLPTRGTAEWLSFDVTDTVREWLLRRESNLGLEISI 175

Qy 222 HCSC-----DSKDNTLHVEINGFNS---GRRGDLATIHGM---NRPFLLLMATPL 265
 || | :: : : | :: ||| : | |::| |
 Db 176 HCPCHTFQPNGDILENVHEVMEIKFKGVDNEDDHGRGDLGRLKKQKDHHNPHLILMMIPP 235

Qy 266 ERAQHLHSSRRRRALDTSYPYDVPDYASLALDTSNYCFSSTEKNCCVRQLYIDFRKDLGW 325
 | : ||||| : |::| | ||||| : ||||
 Db 236 HRLDSPGQGSQRK-----KRALDTSNYCFRNLEENCCVRPLYIDFRQDLGW 280

Qy 326 KWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVPQALEPLPIVY 385
 ||:|||||:|||| | ||: | || || | ||:||||| ||| |::|
 Db 281 KKWHEPKGYANFCSGPCPYLRSADTTHTSTVLGLYNTLNPEASASPCCVPQDLEPLTILY 340

Qy 386 YVGRKPKVEQLSNMIVRSCKCS 407
 |||| ||||| ||::| ||||
 Db 341 YVGRTPKVEQLSNMVVKSCCKCS 362

RESULT 12

Q98854

ID Q98854 PRELIMINARY; PRT; 361 AA.
 AC Q98854;
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Transforming growth factor beta 2 (TGF-beta 2) (Fragment).
 GN TGFB2.
 OS Cyprinus carpio (Common carp).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Cyprinus.
 OX NCBI_TaxID=7962;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=HEART;
 RX MEDLINE=97354301; PubMed=9210595;
 RA Sumathy K., Desai K.V., Kondaiah P.;
 RT "Isolation of transforming growth factor-beta2 cDNA from a fish,
 RT Cyprinus carpio by RT-PCR.";
 RL Gene 191:103-107(1997).
 CC -!- FUNCTION: TGF-BETA 2 HAS SUPPRESSIVE EFFECTS ON INTERLEUKIN-2
 CC DEPENDENT T-CELL GROWTH.
 CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
 DR EMBL; U66874; AAB62983.1; -.
 DR HSSP; P08112; 2TGI.
 DR InterPro; IPR001839; TGFb.
 DR InterPro; IPR001111; TGFb_N.
 DR InterPro; IPR003911; TGF_TGFb.
 DR Pfam; PF00019; TGF-beta; 1.

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DR      Pfam; PF00688; TGFb_propeptide; 1.
DR      PRINTS; PR01423; TGFBETA.
DR      ProDom; PD000357; TGFB; 1.
DR      SMART; SM00204; TGFB; 1.
DR      PROSITE; PS00250; TGF_BETA_1; 1.
KW      Growth factor; Mitogen; Glycoprotein.
FT      NON_TER      1      1
FT      PROPEP      <1      257
FT      CHAIN      258      361      TRANSFORMING GROWTH FACTOR BETA 2.
FT      DISULFID      264      273      BY SIMILARITY.
FT      DISULFID      272      335      BY SIMILARITY.
FT      DISULFID      334      334      INTERCHAIN (BY SIMILARITY).
FT      CARBOHYD      30      30      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD      98      98      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      CARBOHYD      199      199      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT      NON_TER      361      361
SQ      SEQUENCE      361 AA; 41931 MW; 94D930FA970A3FD3 CRC64;

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Qy	52	QILSKRLASPPSPQGDVPPGP--LPEAVLALYNSTRDRVAGESVEPEPEPE-----ADYY	104
Db	1	QILCKLKLSCPP---EIYPEPEEVSRDIIAIYNSTRDLLQEKANERAATCERQRTGEEYY	57
Qy	105	AKEVTRVLM---VESGNQIYDKFKGTPHSLYMLFNTSELREAVPEPVLLSRAELRLLRL-	160
Db	58	AKEVHKIDMQPFYPAENVIPKHY-NPYFRRLRFDVSSMEKNASN---LVKAELRIFRLQ	113
Qy	161	--KLKV-EQHVELYQ-----KYSNDSWRYLSNRLLAPSDSPEWLSFDVTGVVRQWLTRRE	212
Db	114	NPKARVSEQRIELYQILGHKDLTSPTRQYIDSKVVRTRTEGEWLSFDVTEAVSEWLLHRD	173
Qy	213	AIEGFRLSAHCSC-----DSKDNTHLVEINGFNSG--RRGDLATI---HGMNR	255
Db	174	RNNGFKISLHCPCTFVPSNNYIIPNKSEELARFAGIDDSFVHGGDLKMFKKRRHSGQS	233
Qy	256	PFLLLMATPLERAQHLHSSRHRRALDTNSYPYDVPDYASIALDNTNYCFSSTEKNCCVRQL	315
Db	234	PHLLMLLPSPYRLESQHKSHRQ-----KRALDAAFCFRNVQDNCCLRSL	277
Qy	316	YIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPGASAAPCCVP	375
Db	278	YIDFKKDLGWKWIHEPKGYNANFCAGACPYLWSADTQHSNIGLYNTINPEASASPCCVS	337
Qy	376	QALEPLPIVYYVGRKPKVEQLSNM	399
Db	338	ODLEPLTILYYIGKTPKIEOLSNM	361

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Transforming growth factor beta 1 (TGF-beta 1) (Fragment).
 GN TGFB1.
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 OX NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LVG (SYR);
 RX MEDLINE=93304479; PubMed=8317544;
 RA Wong D.T., Donoff R.B., Yang J., Song B.Z., Matossian K., Nagura N.,
 RA Elovic A., McBride J., Gallagher G., Todd R.;
 RT "Sequential expression of transforming growth factors alpha and beta 1
 RT by eosinophils during cutaneous wound healing in the hamster."
 RL Am. J. Pathol. 143:130-142(1993).
 RN [2]
 RP SEQUENCE OF 26-115 FROM N.A.
 RC STRAIN=SYRIAN; TISSUE=SPLEEN;
 RX MEDLINE=98234044; PubMed=9573100;
 RA Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;
 RT "Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and
 RT analysis of cytokine mRNA expression in experimental visceral
 RT leishmaniasis."
 RL Infect. Immun. 66:2135-2142(1998).
 CC -!- FUNCTION: TGF-BETA 1 IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROLS
 CC PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
 CC TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF
 CC THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1
 CC REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND
 CC DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
 CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
 CC -!- SIMILARITY: TO OTHER GROWTH FACTORS OF THE TGF-BETA FAMILY.
 DR EMBL; X60296; CAA42838.1; -.
 DR EMBL; AF046214; AAC40099.1; -.
 DR HSSP; P01137; 1KLA.
 DR InterPro; IPR001839; TGFb.
 DR Pfam; PF00019; TGF-beta; 1.
 DR ProDom; PD000357; TGFb; 1.
 DR SMART; SM00204; TGFB; 1.
 DR PROSITE; PS00250; TGF_BETA_1; 1.
 KW Growth factor; Mitogen; Glycoprotein.
 FT NON_TER 1 1
 FT PROPEP <1 18
 FT CHAIN 19 130 TRANSFORMING GROWTH FACTOR BETA 1.
 FT DISULFID 25 34 BY SIMILARITY.
 FT DISULFID 33 96 BY SIMILARITY.
 FT DISULFID 66 129 BY SIMILARITY.
 FT DISULFID 95 95 INTERCHAIN (BY SIMILARITY).
 FT CONFLICT 93 93 G -> S (IN REF. 2).
 SQ SEQUENCE 130 AA; 14997 MW; 8B41DD6CF39CCA77 CRC64;

Query Match 31.9%; Score 691.5; DB 11; Length 130;
 Best Local Similarity 86.4%; Pred. No. 6.3e-54;
 Matches 127; Conservative 0; Mismatches 3; Indels 17; Gaps 1;

Qy	261	MATPLERAQHLHSSRRHRRALD	NTSY	PDV	PDY	AS	LA	LD	TN	YCF	S	ST	EK	NC	CV	RQ	LY	ID	FR	320								
Db	1	MATPLERAQHLQSSRHRR	-----												AL	DT	TN	YCF	S	ST	EK	NC	CV	RQ	LY	ID	FR	43
Qy	321	KDLGWKWIHEPKGYHANFCLG	PC	PI	WS	LD	TQ	YS	KV	LA	LY	NQ	HN	PG	SA	AP	CC	VP	QA	LE	P	380						
Db	44	KDLGWKWIHEPKGYHANFCLG	PC	PI	WS	LD	TQ	YS	KV	LA	LY	NQ	HN	PG	SA	AG	PC	CC	VP	QA	LE	P	103					
Qy	381	LP	IV	YV	YV	GR	KP	KV	EQ	LS	NM	IV	RS	CK	KS	407												
Db	104	LP	IV	YV	YV	GR	KP	KV	EQ	LS	NM	IV	RS	YK	KS	130												

095N80

Qy	264	PLERAQHLHSSRRRALDTNSYPYDVPDYASLALDTNYCFSSTEKNCCVRQLYIDFRKDL	323
Db	1	PLERAQHLHSSRQRR-----ALDTNYCFSSTEKNCCVRQLYIDFRKDL	43
Qy	324	GWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPASAAAPCCVPQALEPLPI	383
Db	44	GWKWIHEPKGYHANFCLGPCPYIWSLDTQYSKVLALYNQHNPASAAAPCCVPQALEPLPI	103
Qy	384	VYYVGRKPKVEQLSNMIVRSC	404
Db	104	VYYVGRKPKVEQLSNMIVRSC	124

RESULT 15

O02730

ID O02730 PRELIMINARY; PRT; 112 AA.
AC O02730; O97501;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Transforming growth factor beta 1 (TGF-beta 1) (Fragment).
GN TGFBI OR TGF-BETA-1.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Taylor T.K., James E.R., McGonigle S., Yoho E.R.;
RL Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE OF 2-99 FROM N.A.
RA Inoue K., Kawabe Y., Kodama T.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
CC -!- FUNCTION: TGF-BETA 1 IS A MULTIFUNCTIONAL PEPTIDE THAT CONTROLS
CC PROLIFERATION, DIFFERENTIATION, AND OTHER FUNCTIONS IN MANY CELL
CC TYPES. MANY CELLS SYNTHESIZE TGF-BETA 1 AND ESSENTIALLY ALL OF
CC THEM HAVE SPECIFIC RECEPTORS FOR THIS PEPTIDE. TGF-BETA 1
CC REGULATES THE ACTIONS OF MANY OTHER PEPTIDE GROWTH FACTORS AND
CC DETERMINES A POSITIVE OR NEGATIVE DIRECTION OF THEIR EFFECTS.
CC -!- SUBUNIT: HOMODIMER, DISULFIDE-LINKED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DR EMBL; AF000133; AAB53806.1; -.
DR EMBL; AB020217; BAA36950.1; -.
DR HSSP; P01137; 1KLA.
DR InterPro; IPR002400; GF_cysknot.
DR InterPro; IPR001839; TGFb.
DR Pfam; PF00019; TGF-beta; 1.
DR PRINTS; PR00438; GFCYSKNOT.
DR ProDom; PD000357; TGFb; 1.
DR SMART; SM00204; TGFB; 1.
DR PROSITE; PS00250; TGF_BETA_1; 1.
KW Growth factor; Mitogen; Glycoprotein.
FT NON_TER 1 1
FT CHAIN 1 112 TRANSFORMING GROWTH FACTOR BETA 1.
FT DISULFID 7 16 BY SIMILARITY.
FT DISULFID 15 78 BY SIMILARITY.
FT DISULFID 44 109 BY SIMILARITY.
FT DISULFID 48 111 BY SIMILARITY.
FT DISULFID 77 77 INTERCHAIN (BY SIMILARITY).
FT CONFLICT 2 3 LD -> FS (IN REF. 2).
FT CONFLICT 85 92 PLPIVYYV -> ATAHRVTTL (IN REF. 2).
SQ SEQUENCE 112 AA; 12795 MW; 53C5B7D46355A6F3 CRC64;

Query Match 29.4%; Score 638; DB 6; Length 112;
Best Local Similarity 100.0%; Pred. No. 3.1e-49;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      296 ALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSK 355
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1  ALDTNYCFSSTEKNCCVRQLYIDFRKDLGWKWIHEPKGYHANFCLGPCPYIWSLDTQYSK 60

Qy      356 VLALYNQHNPASAAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 407
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 VLALYNQHNPASAAAPCCVPQALEPLPIVYYVGRKPKVEQLSNMIVRSCKCS 112
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Search completed: October 28, 2003, 09:12:27
Job time : 33.6306 secs